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(54) Title: METHODS FOR IDENTIFYING PATHWAY-SPECIFIC REPORTERS AND TARGET GENES, AND USES THEREOF

(57) Abstract

The present invention relates to methods for identifying one or more reporter genes for a particular biological pathway of interest. The reporter genes of this invention are particularly useful for analyzing the activity of particular biological pathways of interest, and may be further used in the design of drugs, drug therapies or other biological agents (e.g., insecticides, herbicides, fungicides, antibiotics, or antivirals) to target a particular biological pathway. The present invention also relates to methods for identifying one or more target genes for a particular biological pathway of interest. Target genes of the invention are useful as specific targets for drugs which may be designed to enhance, inhibit, or modulate a particular biological pathway. Methods to identify genes which modify the function or structure of a member (e.g., compound or gene product) of a particular biological pathway are provided.

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METHODS FOR IDENTIFYING PATHWAY-SPECIFIC REPORTERS AND TARGET GENES, AND USES THEREOF

5

1. INTRODUCTION

The present invention relates to methods for identifying one or more reporter genes for a particular biological pathway of interest. The reporter genes of this invention are particularly useful for analyzing the activity of particular biological pathways of interest, and may be further used in the design of drugs, drug therapies or other biological agents (*e.g.*, insecticides, herbicides, fungicides, antibiotics, or antivirals) to target a particular biological pathway. The present invention also relates to methods for identifying one or more target genes for a particular biological pathway of interest. Target genes of the invention are useful as specific targets for drug which may be designed to enhance, inhibit, or modulate a particular biological pathway. Methods to identify gene which modifies the function or structure of a member (*e.g.*, compound or gene product) of a particular biological pathway are provided.

The present invention provides examples of reporter genes and/or target genes which have been discovered by the methods of the invention. Specifically, the inventors have made the surprising discovery that five *S. cerevisiae* genes (previously of unknown function) form clustered co-regulated sets of genes and are reporters of the ergosterol-pathway. The methods of the invention are also exemplified in that the inventors have specifically discovered six *S. cerevisiae* reporter genes of the protein kinase C (PKC) pathway. Two of these genes are also novel target genes of the PKC pathway and provide targets for the development of PKC pathway-specific drugs, drug therapies, or other related biological or therapeutical agents. The methods of the invention are further exemplified by the discovery of four novel reporter genes of the *S. cerevisiae* Invasive Growth pathway. One of these genes also serves as a target gene in the Invasive Growth pathway, and may be used to develop Invasive Growth pathway-specific drugs, drug therapies, or other related biological or therapeutical agents.

30

2. BACKGROUND OF THE INVENTION

Citation of a reference herein shall not be construed as an admission that such reference is prior art to the present invention.

35

2.1. MICROARRAY TECHNOLOGY

Within the past decade, several technologies have made it possible to monitor the expression level of a large number of transcripts at any one time (*see, e.g., Schena et al., 1995, Quantitative monitoring of gene expression patterns with a complementary DNA*
5 *micro-array, Science 270:467-470; Lockhart et al., 1996, Expression monitoring by hybridization to high-density oligonucleotide arrays, Nature Biotechnology 14:1675-1680; Blanchard et al., 1996, Sequence to array: Probing the genome's secrets, Nature Biotechnology 14, 1649; U.S. Patent 5,569,588, issued October 29, 1996 to Ashby et al. entitled "Methods for Drug Screening"*). In organisms for which the complete genome is
10 known, it is possible to analyze the transcripts of all genes within the cell. With other organisms, such as human, for which there is an increasing knowledge of the genome, it is possible to simultaneously monitor large numbers of the genes within the cell.

Such monitoring technologies have been applied to the identification of genes which are up regulated or down regulated in various diseased or physiological states,
15 the analyses of members of signaling cellular states, and the identification of targets for various drugs. *See, e.g., Friend and Hartwell, International Publication WO98/38329 dated September 3, 1993; Stoughton and Friend, U.S. Patent Application Serial No. 09/074,983, filed on May 8, 1998; Friend and Hartwell, U.S. Provisional Application Serial No. 60/056,109, filed on August 20, 1997; Friend and Stoughton, U.S. Provisional Application*
20 *Serial Nos. 60/084,742 (filed on May 8, 1998), 60/090,004 (filed on June 19, 1998) and 60/090,046 (filed on June 19, 1998), all incorporated herein by reference for all purposes.*

Levels of various constituents of a cell are known to change in response to drug treatments and other perturbations of the cell's biological state. Measurements of a plurality of such "cellular constituents" therefore contain a wealth of information about the
25 effect of perturbations and their effect on the cell's biological state. Such measurements typically comprise measurements of gene expression levels of the type discussed above, but may also include levels of other cellular components such as, but by no means limited to, levels of protein abundances, or protein activity levels. The collection of such measurements is generally referred to as the "profile" of the cell's biological state.

30 The number of cellular constituents is typically on the order of a hundred thousand for mammalian cells. The profile of a particular cell is therefore typically of high complexity. Any one perturbing agent may cause a small or a large number of cellular constituents to change their abundances or activity levels. Thus, identifying the particular cellular constituents are associated with a particular biological pathway, provides a difficult
35 and challenging task. Additionally, methods in the art do not provide a means by which all of the cellular constituents which are associated with a particular pathway of interest may be

identified. Therefore, there is a need in the art for methods to identify groups of cellular constituents, which are associated with a particular biological pathway.

2.1.1. THE NEED FOR REPORTER GENES

5 In order to monitor and study a particular biological pathway, it is necessary to have a "read-out" or reporter of the pathway that allows measurement of an alteration of the pathway. Many biological pathways, however, do not have reliable reporters associated with them. There is a need in the art for a method to identify reporters for a particular biological pathway of interest. Additionally, there is a need in the art for novel reporter
10 genes which may be assigned to a particular biological pathway. The present invention provides such a reporters and methods of identifying such reporters.

2.1.2. IDENTIFICATION OF TARGETS

Identification of targets for drug development is a laborious process that has
15 had a low rate of success. Accordingly, there is a need in the art for novel targets for the development of novel drugs and therapies against biologic pathogens of interest. There is also a need in the art for novel targets for the development of novel drugs and therapies which can enhance, inhibit, or modulate a particular biological pathway of interest. Additionally, there is a need in the art for a method of screening potential drug targets that
20 affords high throughput and the ability to assess multiple targets simultaneously. The present invention provides such a targets and methods to identify such targets.

2.2. FUNGI AND DISEASE

Fungi are eukaryotic microorganisms comprising a phylogenetic kingdom.
25 The Kingdom Fungi is estimated to contain over 100,000 species and includes species of "yeast", which is the common term for several families of unicellular fungi.

Although fungal infections were once unrecognized as a significant cause of disease, the extensive spread of fungal infections is a major concern in hospitals, health departments and research laboratories. According to a 1988 study nearly 40% of all deaths
30 from hospital-acquired infections were caused by fungi, not bacteria or viruses (Sternberg, S., 1994, Science 266:1632-34).

Immunocompromised patients are particularly at risk of fungal infections. Patients with impaired immune systems due to AIDS, cancer chemotherapy, or those treated with immunosuppressive drugs used to prevent rejection in organ transplant are common
35 hosts for fungal infections. Organisms including *Cryptococcus*, *Candida*, *Histoplasma*, *Coccidioides*, and many as 150 species of fungi have been linked to human or animal

diseases (Sternberg, S., 1994, Science 266:1632-34). Under immunocompromised conditions, fungi that are normally harmless to the host when maintained in the gastrointestinal system, can be transferred to the bloodstream, eyes, brain, heart, kidneys, and other tissues leading to symptoms ranging in severity from white patches on the tongue, to fever, rupturing of the retina, blindness, pneumonia, heart failure, shock, or sudden catastrophic clotting of the blood (Sternberg, S., 1994, Science 266:1632-34). In susceptible burn victims, even baker's yeast, common in the human mouth and normally non-virulent, can lead to severe infection (Sternberg, S., 1994, Science 266:1632-34). Hospital transmission may also occur via catheters or other invasive equipment (Sternberg, S., 1994, Science 266:1632-34).

Fungal infections are not limited to individuals with compromised immune systems. Geological and meteorological events have been reported to trigger fungal outbreaks. Following a 1994 earthquake in California, tremors were estimated to have released infectious fungal spores from the soil triggering a 3-year statewide epidemic that lead to more than 4500 cases per year (Sternberg, S., 1994, Science 266:1632-34). Similarly, environmental cycles of droughts and heavy rains are believed to be associated with release infectious spores leading to epidemic infections (Sternberg, S., 1994, Science 266:1632-34).

The widespread dissipation of fungal infection coupled to the recognition of fungi as a significant disease factor creates an increasing need for antifungal agents. Existing antifungal therapies harbor many disadvantages as discussed in Section 2.1.2, and novel therapies and targets for therapy are needed.

2.2.1. ANTIFUNGAL AGENTS AND NEED FOR IMPROVEMENTS

A useful antifungal agent must be toxic to the parasite, but not to the host. One way to achieve this goal is to target a structure or pathway that is unique to the pathogen. For example, successful antibacterial therapies often take advantage of the differences between the prokaryotic bacteria and the eukaryotic host. However, since fungal pathogens, like human cells, are eukaryotic, it has been more difficult to identify therapeutic agents that are unique to the pathogen. Among the targets exploited to date are the biochemical pathways for (1) membrane integrity; (2) ergosterol synthesis (reviewed in *Handbook of Experimental Pharmacology*, 1990, Springer-Verlag, Heidelberg, JF Ryley, eds.); (3) nucleic acid synthesis; and (4) cell wall synthesis.

However, antifungal agents and drugs currently used to treat fungal pathogens are lacking in both efficacy and safety. To date, only a limited number of therapeutic agents are available for the treatment of fungal infections. These drugs,

however, often prove to be toxic to the host, or are accompanied by severe side effects. The commonly prescribed drug, Amphotericin B, a mainstay of antifungal therapy, includes such side effects as fever, chills, low blood pressure, headache, nausea, vomiting, inflammation of blood vessels and kidney damage (Sternberg, S., 1994, Science 266:1632-34). Further, many of the existing therapies act to inhibit or slow fungal growth, but do not kill the infecting fungi.

3. SUMMARY OF THE INVENTION

The present invention relates to methods for identifying one or more reporter genes for a particular biological pathway of interest. The reporter genes of this invention are particularly useful for analyzing the activity of particular biological pathways of interest, and may be further used in the design of drugs, drug therapies or other biological agents (e.g., insecticides, herbicides, fungicides, antibiotics, or antivirals) to target a particular biological pathway. The present invention also relates to methods for identifying one or more target genes for a particular biological pathway of interest. Target genes of the invention are useful as specific targets for drug which may be designed to enhance, inhibit, or modulate a particular biological pathway. Methods to identify gene which modifies the function or structure of a member (e.g., compound or gene product) of a particular biological pathway are provided.

The present invention provides examples of reporter genes and/or target genes which have been discovered by the methods of the invention. Specifically, the inventors have made the surprising discovery that five *S. cerevisiae* genes (previously of unknown function) form clustered co-regulated sets of genes and are reporters of the ergosterol-pathway. The methods of the invention are also exemplified in that the inventors have specifically discovered six *S. cerevisiae* reporter genes of the protein kinase C (PKC) pathway. Two of these genes are also novel target genes of the PKC pathway and provide targets for the development of PKC pathway-specific drugs, drug therapies, or other related biological or therapeutical agents. The methods of the invention are further exemplified by the discovery of four novel reporter genes of the *S. cerevisiae* Invasive Growth pathway. One of these genes also serves as a target gene in the Invasive Growth pathway, and may be used to develop Invasive Growth pathway-specific drugs, drug therapies, or other related biological or therapeutical agents.

The invention provides a method of identifying a reporter gene for a particular biological pathway in a cell comprising identifying a gene which clusters to a geneset associated with the biological pathway, wherein said gene which clusters to the geneset associated with the particular biological pathway is a reporter gene.

In one embodiment the geneset associated with the particular biological pathway is identified by a method comprising identifying one or more genes in a geneset which are associated with the particular biological pathway, wherein said geneset having one or more genes associated with the particular biological pathway is a geneset associated with the particular biological pathway.

In another embodiment the geneset associated with the particular biological pathway is identified by identifying a geneset which is activated or inhibited by perturbations which target the biological pathway, wherein a geneset which is activated or inhibited by perturbations which target the biological pathway is a geneset associated with the particular biological pathway.

In one embodiment the method further comprises identifying a gene which clusters specifically to a geneset associated with the particular biological pathway, wherein said gene which clusters specifically to the geneset associated with the particular biological pathway is a reporter gene.

In one embodiment the reporter gene is further identified as a gene whose expression is not altered by perturbations which effect other biological pathways, said other biological pathways being different from said particular biological pathway.

In another embodiment the geneset is provided by a method comprising: (a) measuring changes in expression of a plurality of genes in the cell in response to a plurality of perturbations to the cell; and (b) grouping or re-ordering said plurality of genes into one or more co-varying sets, wherein said one or more co-varying sets comprise said geneset. In a further embodiment said plurality of genes are grouped or re-ordered into one or more co-varying sets by means of a pattern recognition algorithm. In another embodiment the clustering algorithm analyzes arrays or matrices, said arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell, wherein said analysis determines dissimilarities between individual genes.

In one embodiment the plurality of perturbations to the cell are also grouped or re-ordered according to their similarity. In another embodiment said plurality of perturbations to the cell are grouped or re-ordered by means of a pattern recognition algorithm. In a further embodiment the pattern recognition algorithm is a clustering algorithm.

In one embodiment of the invention, the clustering algorithm analyzes arrays or matrices, said arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell. In

another embodiment the reporter gene is further identified as has a high level of induction. In another embodiment the expression of the reporter gene is further identified to change by at least a factor of two in response to perturbations of the particular biological pathway.

In a further embodiment expression of the reporter gene is further identified to change by at least a factor of 10 in response to perturbations to the particular biological pathway. In another embodiment the expression of the reporter gene is further identified to change by at least a factor of 100 in response to perturbations to the particular biological pathway.

In one embodiment the expression of the reporter gene is further identified to change in response to slight perturbations to the particular biological pathway.

In another embodiment the perturbation to the particular biological pathway comprises exposure to a drug, and said reporter gene is further identified to change in response to low levels of exposure to the drug.

In one embodiment the reporter gene is further identified to respond to perturbations targeted to the entire particular biological pathway. In one embodiment the reporter gene is further identified to respond to perturbations directed to one or more portions of the particular biological pathway. In another embodiment the reporter gene is further identified to respond to perturbations targeted to early steps of the particular biological pathway. In another embodiment the reporter gene is further identified to respond to perturbations targeted to late steps of the particular biological pathway. In yet another embodiment the reporter gene is further identified by identifying a gene which kinetically induces quickly in response to perturbations to the particular biological pathway.

In another embodiment the reporter gene is further identified by identifying a gene which reaches steady state within about eight hours after a perturbation to the particular biological pathway. In a further embodiment the reporter gene is further identified by identifying a gene which reaches steady state within about six hours after a perturbation to the particular biological pathway. In another embodiment the reporter gene is further identified by identifying a gene which is induced within about two hours after a perturbation to the particular biological pathway.

In still another embodiment the reporter gene is further identified by identifying a gene which is induced within about 90 minutes after a perturbation to the particular biological pathway. In another embodiment the reporter gene is further identified by identifying a gene which is induced within about 60 minutes after a perturbation to the particular biological pathway. In a further embodiment the reporter gene is further identified by identifying a gene which is induced within about 30 minutes after a perturbation to the particular biological pathway. In one embodiment the reporter gene is

further identified by identifying a gene which is induced within about 10 minutes after a perturbation to the particular biological pathway. In another embodiment the reporter gene is further identified by identifying a gene which is induced within about 7 minutes after a perturbation to the particular biological pathway.

5 The invention provides a method of identifying a target gene for a particular biological pathway in a cell comprising identifying a gene which clusters to a geneset associated with the particular biological pathway, wherein said gene which clusters to a geneset associated with the particular biological pathway and is identified as a gene which is necessary for normal function of said particular biological pathway.

10 In one embodiment the geneset associated with the particular biological pathway is identified by a method comprising identifying one or more genes in a geneset which are associated with the particular biological pathway, wherein said geneset having one or more genes associated with the particular biological pathway is a geneset associated with the particular biological pathway. In another embodiment the geneset associated with
15 the particular biological pathway is identified by identifying a geneset which is activated or inhibited by perturbations which target the biological pathway, wherein a geneset which is activated or inhibited by perturbations which target the biological pathway is a geneset associated with the particular biological pathway.

 In one embodiment the genesets are provided by a method comprising:(a)
20 measuring changes in expression of a plurality of genes in the cell in response to a plurality of perturbations to the cell; and (b) grouping or re-ordering said plurality of genes into one or more co-varying sets, wherein said one or more co-varying sets comprise said genesets.

 In one embodiment said plurality of genes are grouped or re-ordered into one or more co-varying sets by means of a pattern recognition algorithm. In another
25 embodiment the pattern recognition algorithm is a clustering algorithm.

 In one embodiment the clustering algorithm analyzes arrays of matrices, said arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell, wherein said analysis determines dissimilarities between individual genes.

30 In one embodiment the plurality of perturbations to the cell are also grouped or re-ordered according to their similarity. In another embodiment the plurality of perturbations to the cell are grouped or re-ordered by means of a pattern recognition algorithm.

 In one embodiment the pattern recognition algorithm is a clustering
35 algorithm. In another embodiment the clustering algorithm analyzes arrays of matrices, said

arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell.

In one embodiment the reporter gene is a reporter for the ergosterol-pathway, and the reporter gene is selected from the group consisting of:

- 5 YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9).

- In another embodiment the reporter gene is a reporter for the PKC-pathway,
- 10 and the reporter gene is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19),
- 15 and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21).

- In another embodiment the reporter gene is a reporter for the Invasive Growth pathway, and the reporter gene selected from the group consisting of
- KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23),
- PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as
- 20 depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

- In another embodiment the biological pathway is selected from the group consisting of: a signaling pathway, a control pathway, a mating pathway, a cell cycle pathway, a cell division pathway, a cell repair pathway, a small molecule synthesis
- 25 pathway, a protein synthesis pathway, a DNA synthesis pathway, a RNA synthesis pathway, a DNA repair pathway, a stress-response pathway, a cytoskeletal pathway, a steroid pathway, a receptor-mediated signal transduction pathway, a transcriptional pathway, a translational pathway, an immune response pathway, a heat-shock pathway, a motility pathway, a secretion pathway, an endocytotic pathway, a protein sorting pathway, a
- 30 phagocytic pathway, a photosynthetic pathway, an excretion pathway, an electrical response pathway, a pressure-response pathway, a protein modification pathway, a small-molecule response pathway, a toxic-molecule response pathway, and a transformation pathway.

- In one embodiment the target gene of the PKC-pathway is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID
- 35 NO:11), and YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13).

The invention provides a method for determining whether a molecule affects the function or activity of an ergosterol pathway in a cell comprising: (a) contacting the cell with, or recombinantly expressing within a cell the molecule; and (b) determining whether the expression of one or more of the genes selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9) is changed relative to said expression in the absence of the molecule. In a further embodiment the method is a method for determining whether the molecule inhibits ergosterol synthesis such that a cell contacted with the molecule exhibits a lower level of ergosterol than a cell which is not contacted with said molecule. In another embodiment step (b) comprises determining whether YPL272c expression increases.

The invention provides a kit comprising in one or more containers a) a substance selected from the group consisting of an antibody against an ergosterol-pathway protein, a gene probe capable of hybridizing to RNA of an ergosterol-pathway gene, and pairs of gene primers capable of priming amplification of at least a portion of an ergosterol-pathway gene, and b) a molecule known to be capable of perturbing the ergosterol pathway.

The invention provides a method for identifying a molecule that activates the ergosterol pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the ergosterol-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9).

The invention provides a method for identifying a molecule that activates the ergosterol pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the ergosterol-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as

depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9). In one embodiment the fungal cell is a transgenic cell.

The invention provides a method for identifying a molecule that modulates
5 the expression of an ergosterol-pathway gene selected from the group consisting of YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9), comprising recombinantly expressing in a
10 fungal cell one or more candidate molecules, and detecting the expression of said ergosterol-pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates ergosterol-pathway gene expression. In one embodiment the fungal cell is a transgenic cell.

The invention provides a method for identifying a molecule that modulates
15 the activity of an ergosterol-pathway protein selected from the group consisting of YHR039C (as depicted in FIG.3, as set forth in SEQ ID NO:2), YLW100W (as depicted in FIG.5, as set forth in SEQ ID NO:4), YPL272C (as depicted in FIG.7, as set forth in SEQ ID NO:6), YGR131W (as depicted in FIG.9, as set forth in SEQ ID NO:8), and YDR453C (as depicted in FIG.11, as set forth in SEQ ID NO:10), comprising contacting a fungal cell
20 with one or more candidate molecules, detecting said protein; wherein an increase or decrease in the protein level relative to the level in the absence of candidate molecules indicates that the molecule modulates ergosterol-pathway gene expression.

The invention provides a method of identifying a molecule that binds to a ligand selected from the group consisting of (i) an *S. cerevisiae* ergosterol-pathway protein
25 selected from the group consisting of YHR039C (as depicted in FIG.3, as set forth in SEQ ID NO:2), YLW100W (as depicted in FIG.5, as set forth in SEQ ID NO:4), YPL272C (as depicted in FIG.7, as set forth in SEQ ID NO:6), YGR131W (as depicted in FIG.9, as set forth in SEQ ID NO:8), and YDR453C (as depicted in FIG.11, as set forth in SEQ ID NO:10), (ii) a fragment of the *S. cerevisiae* ergosterol-pathway protein, and (iii) a nucleic
30 acid encoding the *S. cerevisiae* ergosterol-pathway protein or fragment, the method comprising:(a) contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and (b) identifying a molecule within the plurality that binds to the ligand.

The invention provides a method for determining whether a molecule affects
35 the function or activity of an PKC pathway in a cell comprising:(a) contacting the cell with, or recombinantly expressing within a cell the molecule; and (b) determining whether the

expression of one or more of the genes selected from the group consisting of:
SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C
(as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted
in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in
5 FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set
forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in
SEQ ID NO:21) is changed relative to said expression in the absence of the molecule. In
one embodiment step (b) comprises determining whether SLT2 expression increases.

The invention provides a kit comprising in one or more containers a) a
10 substance selected from the group consisting of an antibody against a PKC-pathway protein,
a gene probe capable of hybridizing to RNA of a PKC-pathway gene, and pairs of gene
primers capable of priming amplification of at least a portion of a PKC-pathway gene, and
b) a molecule known to be capable of perturbing the PKC pathway.

The invention provides a method for identifying a molecule that activates
15 the PKC pathway in yeast comprising contacting a yeast cell with one or more candidate
molecules, and detecting a change in the RNA expression of a reporter gene for the
PKC-pathway relative to the expression of the reporter gene in a yeast cell not contacted by
the one or more candidate molecules, wherein the reporter gene is selected from the group
consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11),
20 YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W)
(as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted
in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set
forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in
SEQ ID NO:21).

25 The invention provides a method for identifying a molecule that activates the
PKC pathway in yeast comprising contacting a yeast cell with one or more candidate
molecules, and detecting a change in the protein expression of a reporter gene for the
PKC-pathway relative to the expression of the reporter gene in a yeast cell not contacted by
the one or more candidate molecules, wherein the reporter gene is selected from the group
30 consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11),
YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W)
(as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted
in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set
forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in
35 SEQ ID NO:21). In one embodiment the fungal cell is a transgenic cell.

The invention provides a method for identifying a molecule that modulates the expression of a PKC-pathway gene selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21), comprising recombinantly expressing in a fungal cell one or more candidate molecules, and detecting the expression of said PKC-pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates PKC-pathway gene expression. In one embodiment the fungal cell is a transgenic cell.

The invention provides a method for identifying a molecule that modulates the activity of a PKC-pathway protein selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.18, as set forth in SEQ ID NO:12), YKR161C (as depicted in FIG.20, as set forth in SEQ ID NO:14), PIR3(YKL163W) (as depicted in FIG.22, as set forth in SEQ ID NO:16), YPK2(YMR104C) (as depicted in FIG.24, as set forth in SEQ ID NO:18), YLR194C (as depicted in FIG.26, as set forth in SEQ ID NO:20), and ST1(YDR055W) (as depicted in FIG.28, as set forth in SEQ ID NO:22), comprising contacting a fungal cell with one or more candidate molecules, detecting said protein; wherein an increase or decrease in the protein level relative to the level in the absence of candidate molecules indicates that the molecule modulates PKC-pathway gene expression.

The invention provides a method of identifying a molecule that binds to a ligand selected from the group consisting of (i) an *S. cerevisiae* PKC-pathway protein selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.18, as set forth in SEQ ID NO:12), YKR161C (as depicted in FIG.20, as set forth in SEQ ID NO:14), PIR3(YKL163W) (as depicted in FIG.22, as set forth in SEQ ID NO:16), YPK2(YMR104C) (as depicted in FIG.24, as set forth in SEQ ID NO:18), YLR194C (as depicted in FIG.26, as set forth in SEQ ID NO:20), and ST1(YDR055W) (as depicted in FIG.28, as set forth in SEQ ID NO:22), (ii) a fragment of the *S. cerevisiae* PKC-pathway protein, and (iii) a nucleic acid encoding the *S. cerevisiae* PKC-pathway protein or fragment, the method comprising: (a) contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and (b) identifying a molecule within the plurality that binds to the ligand.

The invention provides a method for determining whether a molecule affects the function or activity of an *S. cerevisiae* Invasive Growth pathway in a cell comprising:

(a) contacting the cell with, or recombinantly expressing within a cell the molecule; and (b) determining whether the expression of one or more of the genes selected from the group consisting of: KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29), is changed relative to said expression in the absence of the molecule. In one embodiment, step (b) comprises determining whether KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), expression increases.

10 The invention provides a kit comprising in one or more containers a) a substance selected from the group consisting of an antibody against an *S. cerevisiae* Invasive Growth pathway protein, a gene probe capable of hybridizing to RNA of an Invasive Growth pathway gene, and pairs of gene primers capable of priming amplification of at least a portion of an Invasive Growth pathway gene, and b) a molecule known to be
15 capable of perturbing the Invasive Growth pathway.

The invention provides a method for identifying a molecule that activates the Invasive Growth pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the Invasive Growth pathway relative to the expression of the reporter gene in a yeast cell
20 not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

25 The invention provides a method for identifying a molecule that activates the Invasive Growth pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the Invasive Growth pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected
30 from the group consisting of: KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29). In one embodiment the fungal cell is a transgenic cell.

35 The invention provides a method for identifying a molecule that modulates the expression of an Invasive Growth pathway gene selected from the group consisting of

KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23),
 PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as
 depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in
 FIG.35, as set forth in SEQ ID NO:29), comprising recombinantly expressing in a fungal
 5 cell one or more candidate molecules, and detecting the expression of said Invasive Growth
 pathway gene; wherein an increase or decrease in the gene expression relative to the
 expression in the absence of candidate molecules indicates that the molecules modulates
 Invasive Growth pathway gene expression. In one embodiment the fungal cell is a
 transgenic cell.

10 The invention provides a method for identifying a molecule that modulates
 the activity of an Invasive Growth pathway protein selected from the group consisting of
 KSS1(YGR040W) (as depicted in FIG.30, as set forth in SEQ ID NO:24),
 PGU1(YJR153W) (as depicted in FIG.32, as set forth in SEQ ID NO:26), YRL042C (as
 depicted in FIG.34, as set forth in SEQ ID NO:28), and SVS1(YPL163C) (as depicted in
 15 FIG.36, as set forth in SEQ ID NO:30), comprising contacting a fungal cell with one or
 more candidate molecules, detecting said protein; wherein an increase or decrease in the
 protein level relative to the level in the absence of candidate molecules indicates that the
 molecule modulates Invasive Growth pathway gene expression.

The invention provides a method of identifying a molecule that binds to a
 20 ligand selected from the group consisting of (i) an *S. cerevisiae* Invasive Growth pathway
 protein selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.30, as
 set forth in SEQ ID NO:24), PGU1(YJR153W) (as depicted in FIG.32, as set forth in SEQ
 ID NO:26), YRL042C (as depicted in FIG.34, as set forth in SEQ ID NO:28), and
 SVS1(YPL163C) (as depicted in FIG.36, as set forth in SEQ ID NO:30), (ii) a fragment of
 25 the *S. cerevisiae* Invasive Growth pathway protein, and (iii) a nucleic acid encoding the *S.*
cerevisiae Invasive Growth pathway protein or fragment, the method comprising (a)
 contacting the ligand with a plurality of molecules under conditions conducive to binding
 between the ligand and the molecules; and (b) identifying a molecule within the plurality
 that binds to the ligand.

30

4. BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 Schematic diagram of the method by which reporter genes and/or
 target genes are identified

35 FIG. 2 DNA sequence of *S. cerevisiae* YHR039C ergosterol-pathway gene.
 The nucleic acid sequence of YHR039C is set forth in SEQ ID NO:1.

FIG. 3 The amino acid sequence of the protein encoded by *S. cerevisiae* YHR039C ergosterol-pathway gene. The amino acid sequence of YHR039C is set forth in SEQ ID NO:2.

5 FIG. 4 DNA sequence of *S. cerevisiae* YLR100W ergosterol-pathway gene. The nucleic acid sequence of YLR100W is set forth in SEQ ID NO:3.

FIG. 5 The amino acid sequence of the protein encoded by *S. cerevisiae* YLR100W ergosterol-pathway gene. The amino acid sequence of YLR100W is set forth in
10 SEQ ID NO:4.

FIG. 6 DNA sequence of *S. cerevisiae* YPL272C ergosterol-pathway gene. The nucleic acid sequence of YPL272C is set forth in SEQ ID NO:5.

15 FIG. 7 The amino acid sequence of the protein encoded by *S. cerevisiae* YPL272C ergosterol-pathway gene. The amino acid sequence of YPL272C is set forth in SEQ ID NO:6.

FIG. 8 DNA sequence of *S. cerevisiae* YGR131W ergosterol-pathway gene.
20 The nucleic acid sequence of YGR131W is set forth in SEQ ID NO:7.

FIG. 9 The amino acid sequence of the protein encoded by *S. cerevisiae* YGR131W ergosterol-pathway gene. The amino acid sequence of YGR131W is set forth in SEQ ID NO: 8.

25 FIG. 10 DNA sequence of *S. cerevisiae* YDR453C ergosterol-pathway gene. The nucleic acid sequence of YDR453C is set forth in SEQ ID NO:9.

FIG. 11 The amino acid sequence of the protein encoded by *S. cerevisiae*
30 YDR453C ergosterol-pathway gene. The amino acid sequence of YDR453C is set forth in SEQ ID NO:10.

FIG. 12 Ergosterol Biosynthetic Pathway. The various steps in the synthesis of ergosterol in *S. cerevisiae* are shown, beginning with 2 acetyl-CoA. The genes encoding
35 enzymes in the pathway are shown in green. Antifungal agents that inhibit specific steps in the pathway are shown in bold.

FIG. 13 Clotrimazole Titration Plot. This plot shows the complexity of the drug signature and demonstrates genes which are induced or repressed in response to drug treatment. An example of a gene which is induced to a high level is labeled YPL272C.

- 5 FIG. 14 Cluster analysis of ergosterol-pathway genes. When the signature of yeast mutant strains deleted in a number of ergosterol-pathway genes are compared certain the genes cluster on the same branch. The genes Y4R039C, YLR100W, and YGL001C co-clustered and are reporters of the ergosterol-pathway. The genes YPL272C, YGR131W, and YDR453C co-clustered and are also reporters of the ergosterol-pathway.
- 10 Clustering analysis of yeast genes reveals relationships between different genes, and demonstrates that several genes behave similarly to several known ERG genes.

FIG. 15 PKC pathway of yeast as induced by pheromone or cell wall integrity stimulus.

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FIG. 16 Results of two-dimensional cluster analysis which was used in to identify the reporter genes and target genes of the PKC pathway.

FIG. 17A-B DNA sequence of *S. cerevisiae* SL2(YHR030C) PKC-pathway
20 gene. The nucleic acid sequence of SL2(YHR030C) is set forth in SEQ ID NO:11.

FIG. 18 The amino acid sequence of the protein encoded by *S. cerevisiae* SL2(YHR030C) PKC-pathway gene. The amino acid sequence of SL2(YHR030C) is set forth in SEQ ID NO:12.

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FIG. 19A-B DNA sequence of *S. cerevisiae* YKL161C PKC-pathway gene. The nucleic acid sequence of YKL161C is set forth in SEQ ID NO:13.

FIG. 20 The amino acid sequence of the protein encoded by *S. cerevisiae*
30 YKL161C PKC-pathway gene. The amino acid sequence of YKL161C is set forth in SEQ ID NO:14.

FIG. 21A-B DNA sequence of *S. cerevisiae* PIR3(YKL163W) PKC-pathway gene. The nucleic acid sequence of PIR3(YKL163W) is set forth in SEQ ID
35 NO:15.

FIG. 22 The amino acid sequence of the protein encoded by *S. cerevisiae* PIR3(YKL163W) PKC-pathway gene. The amino acid sequence of PIR3(YKL163W) is set forth in SEQ ID NO:16.

5 FIG. 23A-B DNA sequence of *S. cerevisiae* YPK2(YMR104C) PKC-pathway gene. The nucleic acid sequence of YPK2(YMR104C) is set forth in SEQ ID NO:17.

FIG. 24 The amino acid sequence of the protein encoded by *S. cerevisiae* YPK2(YMR104C) PKC-pathway gene. The amino acid sequence of YPK2(YMR104C) is set forth in SEQ ID NO:18.

FIG. 25A-B DNA sequence of *S. cerevisiae* YLR194C PKC-pathway gene. The nucleic acid sequence of YLR194C is set forth in SEQ ID NO:19.

15 FIG. 26 The amino acid sequence of the protein encoded by *S. cerevisiae* YLR194C PKC-pathway gene. The amino acid sequence of YLR194C is set forth in SEQ ID NO:20.

20 FIG. 27A-B DNA sequence of *S. cerevisiae* PST1(YDR055C) PKC-pathway gene. The nucleic acid sequence of PST1(YDR055C) is set forth in SEQ ID NO:21.

FIG. 28 The amino acid sequence of the protein encoded by *S. cerevisiae* PST1(YDR055C) PKC-pathway gene. The amino acid sequence of PST1(YDR055C) is set forth in SEQ ID NO:22.

FIG. 29 DNA sequence of *S. cerevisiae* KSS1(YGR040W) Invasive Growth pathway gene. The nucleic acid sequence of KSS1(YGR040W) is set forth in SEQ ID NO:23.

FIG. 30 The amino acid sequence of the protein encoded by *S. cerevisiae* KSS1(YGR040W) Invasive Growth pathway gene. The amino acid sequence of KSS1(YGR040W) is set forth in SEQ ID NO:24.

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FIG. 31 DNA sequence of *S. cerevisiae* PGU1(YJR153W) Invasive Growth pathway gene. The nucleic acid sequence of PGU1(YJR153W) is set forth in SEQ ID NO:25.

5 FIG. 32 The amino acid sequence of the protein encoded by *S. cerevisiae* PGU1(YJR153W) Invasive Growth pathway gene. The amino acid sequence of PGU1(YJR153W) is set forth in SEQ ID NO:26.

FIG. 33 DNA sequence of *S. cerevisiae* YHR042C Invasive Growth
10 pathway gene. The nucleic acid sequence of YHR042C is set forth in SEQ ID NO:27.

FIG. 34 The amino acid sequence of the protein encoded by *S. cerevisiae* YHR042C Invasive Growth pathway gene. The amino acid sequence of YHR042C is set forth in SEQ ID NO:28.

15 FIG. 35 DNA sequence of *S. cerevisiae* SVS1(YPL163C) Invasive Growth pathway gene. The nucleic acid sequence of SVS1(YPL163C) is set forth in SEQ ID NO:29.

20 FIG. 36 The amino acid sequence of the protein encoded by *S. cerevisiae* SVS1(YPL163C) Invasive Growth pathway gene. The amino acid sequence of SVS1(YPL163C) is set forth in SEQ ID NO:30.

5. DETAILED DESCRIPTION OF THE INVENTION

25 The present invention relates, in part, to methods for identifying one or more reporter genes and/or target genes for a particular biological pathway of interest. The reporter genes of this invention are particularly useful for analyzing the activity of particular biological pathways of interest, and may be further used in the design of drugs, drug
30 therapies or other biological agents (*e.g.*, insecticides, herbicides, fungicides, antibiotics or antivirals) to target a particular biological pathway. The present invention also relates to methods for identifying one or more target genes for a particular biological pathway of interest. Target genes of the invention are useful as specific targets for drug which may be designed to enhance, inhibit, or modulate a particular biological pathway. Methods to
35 identify gene which modifies the function or structure of a member (*e.g.*, compound or gene product) of a particular biological pathway are provided.

The present invention provides examples of reporter genes and/or target genes which have been discovered by the methods of the invention. Specifically, the inventors have made the surprising discovery that five *S. cerevisiae* genes (previously of unknown function) form clustered co-regulated sets of genes and are reporters of the ergosterol-pathway. The methods of the invention are also exemplified in that the inventors have specifically discovered six *S. cerevisiae* reporter genes of the protein kinase C (PKC) pathway. Two of these genes are also novel target genes of the PKC pathway and provide targets for the development of PKC pathway-specific drugs, drug therapies, or other related biological or therapeutical agents. The methods of the invention are further exemplified by the discovery of four novel reporter genes of the *S. cerevisiae* Invasive growth pathway. One of these genes also serves as a target gene for the Invasive Growth pathway, and may be used to develop Invasive Growth pathway-specific drugs, drug therapies, or other related biological or therapeutical agents.

As described herein, the inventors developed a strategy to search the genome of an organism for cellular constituents which function in a biological pathway of interest. Specifically, the inventors have developed a strategy to search the genome of an organism for reporter genes and/or target genes of a biological pathway of interest. In one embodiment, as described herein, the inventors developed a strategy to search the genome of *S. cerevisiae* for genes which function in a biological pathway of interest. Any pathway of interest may be examined by the methods of the invention. In specific embodiments, the methods of the invention are illustrated by way of the ergosterol-pathway, the PKC pathway, and the Invasive-Growth pathway. Additionally, the genome of any species may be used in the methods of the invention, so long as the genome of the species is at least partially sequenced. In several embodiments of the invention, 20-30%, 30-40%, or 40-60%, of the sequence of the genome of the species examined by the methods of the invention is known. In preferred embodiments of the invention, 60-75%, 75-85%, or 85-90%, of the sequence of the genome of the species examined by the methods of the invention is known. In highly preferred embodiments of the invention, 90-95%, 95-98%, or 98% or more of the sequence of the genome of the species examined by the methods of the invention is known. In a most preferred embodiment of the invention, the entire sequence of the genome of the species examined by the methods of the invention is known.

The methods described herein relate to DNA microarray technology as described in Section 5.1 *et seq.*, and in U.S. Patent serial No. 09/179,569, filed October 27, 1998 now pending, and U.S. Patent serial No. 09/220,275 filed December 23, 1998, now pending, and U.S. Patent serial No. 09/220,142, filed December 23, 1998 now pending, which are incorporated herein by reference in their entirety. The reporter genes and target

genes of the invention constitute very useful tools for probing the function, regulation, activation, and inhibition of their corresponding pathways. Biochemical and genetic analysis of pathways involving the reporters and particularly the targets of the invention can be expected to lead to the discovery of new drug targets, therapeutic proteins, diagnostics, and prognostics useful in the treatment of diseases and clinical problems, for example, those associated with the activation or inactivation of a particular pathway.

Methods for biochemical analysis of pathways of the invention are provided. Such methods may yield results of importance to human disease. For example, systematic identification of participants in the ergosterol-pathway, or components regulating synthesis of ergosterol provide leads to the identification of drug targets, therapeutic proteins, diagnostics, or prognostics useful for treatment or management of fungal infections.

The invention is illustrated by way of examples set forth in Section 6 below which disclose, *inter alia*, the characterization of reporters and targets of the invention including reporter genes of the *S. cerevisiae* ergosterol-pathway, PKC-pathway, and Invasive Growth pathway using DNA microarray technology.

For clarity of disclosure, and not by way of limitation, the detailed description of the invention is divided into the subsections which follow.

5.1. CHARACTERIZATION PROCEDURES

The present invention relates, in part, to methods for identifying one or more reporter genes for a particular biological pathway of interest. As used herein, a reporter gene refers to any gene for which a change in its expression and/or activity of its encoded RNA or protein is indicative of a change in the activity of a particular biological pathway of interest. Thus, the reporter genes of this invention are useful for analyzing the activity of particular biological pathways of interest, *e.g.*, in the design of drugs, drug therapies or other biological agents (*e.g.*, insecticides, herbicides, fungicides, antibiotics or antivirals) to target particular biological pathways.

The present invention also relates, in part, to methods for identifying one or more target genes for a particular biological pathway of interest. As used herein, a target gene refers to any gene whose expression and/or activity is necessary for normal activity or function of the pathway. Thus, the target genes of this invention are useful as targets for drugs designed to enhance, inhibit, or modulate a particular biological pathway. Thus, the target genes of this invention are useful targets for design of drugs, drug therapies or other biological agents (*e.g.*, insecticides, herbicides, fungicides, antibiotics or antivirals) directed to a particular biological pathway.

Biological pathways, as used herein, refer to collections of cellular constituents (*e.g.*, protein abundances or activities, protein phosphorylation, RNA species abundances such as mRNA species abundances, or DNA species abundances such as abundances of cDNA species derived from mRNA -- as used herein the term "cellular constituent" is not intended to refer to known subcellular organelles such as mitochondria, lysozomes, *etc.*) which are related in that each cellular constituent in the collection is influenced according to some biological mechanism by one or more other cellular constituents in the collection. Biological pathways of the present invention therefore include well-known biochemical synthetic pathways including, for example, the yeast ergosterol pathway, in which, *e.g.*, molecules are broken down to provide cellular energy stores or in which protein or nucleic acid precursors or other cellular compounds are synthesized. Signaling and control pathways typically include primary or intermediate signaling molecules, as well as proteins participating in the signal or control cascades usually characterizing these pathways. In signaling pathways, binding of a signal molecule to a receptor usually directly influences the abundances of intermediate signaling molecules and indirectly influences, *e.g.*, the degree of phosphorylation (or other modification) of pathway proteins. Both of these effects in turn influence activities of cellular proteins that are key effectors of the cellular processes initiated by the signal, for example, by affecting the transcriptional state of the cell. Control pathways, such as those controlling the timing and occurrence of the cell cycle, are similar. Here, multiple, often ongoing, cellular events are temporally coordinated, often with feedback control, to achieve a consistent outcome, such as cell division with chromosome segregation. This coordination is a consequence of functioning of the pathway, often mediated by mutual influences of proteins on each other's degree of phosphorylation or other modification. Biological pathways of the invention also include, but are not limited to: signaling pathways, control pathways, mating pathways, cell cycle pathways, cell division pathways, cell repair pathways, small molecule synthesis pathways, protein synthesis pathways, DNA synthesis pathways, RNA synthesis pathways, DNA repair pathways, stress-response pathways, cytoskeletal pathways, steroid pathways, receptor-mediated signal transduction pathways, transcriptional pathways, translational pathways, immune response pathways, heat-shock pathways, motility pathways, secretion pathways, endocytotic pathways, protein sorting pathways, phagocytic pathways, photosynthetic pathways, excretion pathways, electrical response pathways, pressure-response pathways, protein modification pathways, small-molecule response pathways, toxic-molecule response pathway transformation pathways, *etc.* Specifically, the invention herein is illustrated in subsection 6, by way of reporter genes which have been discovered for the ergosterol-pathway and the protein kinase C pathway. Other, well known control

pathways seek to maintain optimal levels of cellular metabolites in the face of a fluctuating environment. Further examples of cellular pathways operating according to understood mechanisms are well known and will therefore be readily apparent to those of skill in the art.

5 The methods of the invention may be used to identify reporter genes or target genes in any cell type from any species of organism. In one preferred embodiment, the methods of the invention are used to identify reporter genes and target genes in *S. cerevisiae*. However, in other preferred embodiments the methods of the invention are used to identify reporter genes and/or target genes in other cell types including prokaryotic and
10 eukaryotic, vertebrate and invertebrate, and in other species, including plant, animal, insect, worm, fungus, yeast, fish, and bird species. In one preferred embodiment the methods of the invention identify one or more reporter genes and or target genes in a mammalian species of interest (*e.g.* mouse, rat, rabbit, dog, cat, horse, sheep, pig, cattle, *etc.*). In one particularly preferred embodiment, the methods of the invention identify one or more reporter genes
15 and/or target genes in a human. In another preferred embodiment the methods of the invention identify one or more reporter genes and/or target genes in a species which is amenable to genetic manipulation of the entire organism (*e.g.*, fly or worm). In other embodiments, the methods of the invention identify one or more reporter genes and/or target genes in other species described herein.

20 The reporter genes of the present invention comprise genes whose genetic transcripts (*i.e.*, mRNA transcripts or cDNA molecules produced from mRNA transcripts) "co-vary" and/or are "co-regulated." Specifically, the reporter genes of the invention increase or decrease the abundance of their transcripts under some set of conditions which is associated with a particular biological pathway of interest and/or with other genes which are
25 associated with the particular biological pathway of interest.

 The target genes of the present invention comprise genes whose genetic transcripts (*i.e.*, mRNA transcripts or cDNA molecules produced from mRNA transcripts) "co-vary" and/or are "co-regulated." Specifically, the target genes of the invention increase or decrease the abundance of their transcripts under some set of conditions which is
30 associated with a particular biological pathway of interest and/or with other genes which are associated with the particular biological pathway of interest. Further, target genes of the invention are those genes of a geneset whose expression and/or activity are necessary for the activity or function of the pathway. Methods for identifying such co-varying genes are described generally and in detail in U.S. patent application serial no. 09/179,569, filed
35 October 27, 1998, now pending, in U.S. patent application serial no. 09/220,275, filed December 23, 1998, now pending, and in U.S. patent application serial no. 09/220,142 filed

December 23, 1998, now pending each of which are incorporated herein by reference in their entirety. These methods are described below as they particularly pertain to identifying reporter genes. Specifically, subsection 5.1.1 describes methods such as cluster analysis which may be used to identify covarying genesets. Such cluster analysis methods are preferably applied to measurements of the "transcriptional state" of a cell; *i.e.*, to measurements of abundances of genetic transcripts (mRNA or cDNA) of a cell. Most preferably, the transcriptional state of a cell is measured using polynucleotide microarrays. Accordingly, subsection 5.1.2-5.1.5 describe methods of measuring the transcriptional state using microarrays, including methods of construction microarrays, methods of hybridizing polynucleotide samples (*e.g.*, from cells) to microarrays, and signal detection on microarrays. Subsection 5.1.6 describes other, less preferred methods by which the transcriptional state of a cell may be measured.

Although for simplicity the disclosure often makes reference to single cells (*e.g.*, "RNA is isolated from a cell exposed to a particular drug"), it will be understood by those of skill in the art that more often any particular step of the invention will be carried out using a plurality of genetically similar cells, *e.g.*, from a cultured cell line. Such similar cells are referred to herein as a "cell type." Such cells may be either from naturally single celled organisms (*e.g.*, *E. coli* or *S. cerevisiae*) or derived from multi-cellular higher organisms (*e.g.* from plant or animal organisms, including mammalian organisms such as a human cell line).

5.1.1. CLUSTER ANALYSIS

In a preferred aspect of the invention, the reporter genes and/or target genes may be identified by methods using cluster analysis. The cluster analysis technique is based in the principal that in general, cellular constituents (*e.g.*, gene transcripts) will respond in a coordinated fashion in response to a particular stimulus, treatment, or biological state. Therefore, subsets of cellular constituents will typically change together, *e.g.*, by increasing or decreasing their abundances and/or activities, under some set of conditions which preferably include the conditions or perturbations of interest to a user of the present invention (*e.g.*, treatment with antifungal compounds).

Further, the abundances and/or activities of individual cellular constituents are not all regulated independently. Rather, individual cellular constituents from a cell will typically share one or more regulatory elements with other cellular constituents from the same cell. For example, and not by way of limitation, in embodiments where the cellular constituents comprise genetic transcripts, the rates of transcription are generally regulated by regulator sequence patterns, *i.e.*, transcription factor binding sites. Typically, several

genes within a cell may share one or more transcription factor binding sites. Such cellular constituents are therefore said to be "co-regulated," and comprise co-regulated cellular constituent sets or "co-regulated sets." For example, and not by way of limitation, genes tend to increase or decrease their rates of transcription together when they possess similar transcription factor binding sites. Such a mechanism accounts for the coordinated responses of genes to particular signaling inputs. For example, see Madhani and Fink, 1998, *Transactions in Genetics* 14:151-155; and Arnone and Davidson, 1997, *Development* 124:1851-1864. For instance, individual genes which synthesize different components of a necessary protein or cellular structure are generally co-regulated. Also, duplicated genes (see, e.g., Wagner, 1996, *Biol. Cybern.* 74:557-567) are co-regulated to the extent that genetic mutations have not led to functional divergence in their regulatory regions. Further, because genetic regulatory sequences are modular (see, e.g., Yuh *et al.*, 1998, *Science* 279:1896-1902), the more regulatory "modules" two genes have in common, the greater the variety of conditions under which they will be co-regulated in their transcription rates. Physical separation between modules along the chromosome is also an important determinant since co-activators are often involved.

In particularly preferred embodiments of the present invention, the cellular constituents in a biological profile comprise genetic transcripts such as mRNA abundances, or abundances of cDNA molecules produced from mRNA transcripts. In such embodiments, the co-regulated sets comprise genes which are generally co-regulated to some extent. Such co-regulated sets are referred to herein as "genesets." Thus, in particularly preferred embodiments of the present invention, the co-regulated cellular constituent sets are genesets. In one specific embodiment of the present invention, the geneset comprises genes of the ergosterol-pathway. In another specific embodiment of the present invention, the geneset comprises genes of the PKC-pathway. In another specific embodiment of the present invention, the geneset comprises genes of the Invasive Growth pathway.

In a specific embodiment of the invention, when the genome of the organism of interest has been sequenced, the number of ORF's can be determined and mRNA coding regions identified by analysis of the DNA sequence. For example, the genome of *Saccharomyces cerevisiae* has been completely sequenced, and is reported to have approximately 6275 ORFs longer than 99 amino acids. Analysis of the ORFs indicates that there are 5885 ORFs that are likely to encode protein products (Goffeau *et al.*, 1996, *Science* 274:546-567). However, many of these genes do not have a known function, nor are they associated with a known function. The invention herein provides methods for assigning function to such ORFs, by the methods of the invention including cluster analysis.

5.2. PATHWAY RESPONSE PROFILES & PERTURBATIONS

In one aspect of the invention, gene expression change in response to a large number of perturbations is used to construct a clustering tree for the purpose of defining genesets. Preferably, the perturbations should target different pathways. In order to
5 measure expression responses to the pathway perturbation, biological samples are subjected to perturbations to pathways of interest. The samples exposed to the perturbation and samples not exposed to the perturbation are used to construct transcript arrays, which are measured to find the mRNAs with modified expression and the degree of modification due to exposure to the perturbation. Thereby, the perturbation-response profile is obtained.

10 FIG. 1 illustrates an overview of the method by which reporter genes and/or target genes are identified. The methods analyze a plurality of "response profiles" which are preferably obtained or provided (FIG. 1, 101) from measurements of the transcriptional or translational state of a cell (*e.g.*, measurements of mRNA abundances or of abundances of cDNA derived from mRNA) under a variety of different experimental conditions. More
15 precisely, the transcriptional or translational state of the cell in response to a plurality of different perturbations to the cell is measured. In preferred embodiments, the transcriptional or translational state of the cell is measured in response to at least ten different perturbations to the cell, more preferably in response to at least 100 perturbations, still more preferably in response to at least 400 perturbations, and yet more preferably in
20 response to over 1,000 different perturbations.

Perturbations to the cell may comprise, for example, exposure to one or more drugs at one or more levels (*i.e.*, at one or more concentrations of the drug). Perturbations may also comprise genetic alterations to the cell such as genetic "knockouts" wherein one or more genes are deleted and/or no longer expressed in the cell. Other possible genetic
25 alterations include regulated expression of one or more genes in the cell, wherein the level of expression of the one or more genes is altered (*e.g.*, increased or decreased) in a controlled manner, *e.g.*, by means of a titratable promoter system. Such perturbations, as well as others which may be used to identify reporter genes and/or target genes, are described, in detail in subsection 5.3 below.

30 Perturbations to the cell may further comprise changes in one or more aspects of the physical environment of the cell. Such environmental changes can include, for example, changes in the temperature (*e.g.*, a temperature elevation of 10 °C) or exposure to moderate doses of radiation. Other exemplary environmental changes include changes in the nutritional environment, such as the presence or absence of particular sugars, amino
35 acids, and so forth.

In preferred embodiments, some of the perturbations are perturbations which are known to affect a particular biological pathway of interest; *i.e.*, the biological pathway for which one or more reporter genes and/or target genes are to be identified. In some preferred embodiments, about 5-50%, preferably about 10-30%, more preferably about 10-25%, still more preferably about 10-20%, and most preferably about 10-15% of the perturbations are perturbations which are known to affect a particular biological pathway of interest.

At least two genes (*i.e.* at least two mRNA or cDNA species) are measured in response to each perturbation. Preferably, at least 10 genes are measured in response to each perturbation, more preferably more than 100 genes, still more preferably more than 1,000 genes, and most preferably more than 10,000 genes. Preferably mRNA or cDNA abundances are measured for more than 10% of the genes of the cell being analyzed. More preferably, mRNA or cDNA abundances are measured for more than 25%, more than 50%, more than 75%, more than 80%, more than 90%, more than 95%, or more than 99% of the genes of the cell being analyzed. Most preferably, mRNA or cDNA abundances are measured for all of the genes of the cell being analyzed. In preferred embodiment, some of the genes measured in response to each perturbation are genes which are known to be involved in a particular biological pathway of interest, *i.e.*, the biological pathway for which one or more reporter genes are to be identified. In some preferred embodiments, about 5-50%, preferably about 10-30%, more preferably about 10-25%, still more preferably about 10-20%, and most preferably about 10-15% of the genes measured in response to each perturbation are genes which are known to be involved in a particular biological pathway of interest.

In preferred embodiments, the response profiles analyzed by the methods of the invention are optionally screened, before the analysis, to select only those cellular constituents that have a significant response in some fraction of the profiles (FIG. 1, 102). In particular, although the profiles may cover up to $\sim 10^5$ genes, in most perturbations a large part or even a majority of these genes will not change significantly, or the changes may be small and dominated by experimental error. Accordingly, in most embodiments, it will be unhelpful and cumbersome to use these genes in to identify reporter genes according to the methods of this invention. Thus, they are preferably deleted from all profiles.

In certain embodiment, only genes that have a response greater than or equal to two standard errors in more than N profiles are selected for subsequent analysis, where N may be one or more and is preferably selected by the user. Preferably, N will tend to be larger for larger sets of response profiles. For example, in one preferred embodiment N may be approximately equal to the square root of the number of response profiles analyzed.

The invention provides a method for determining whether a molecule affects the function or activity of an ergosterol pathway in a cell comprising: (a) contacting the cell with, or recombinantly expressing within a cell the molecule; and (b) determining whether the expression of one or more of the genes selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9) is changed relative to said expression in the absence of the molecule.

The invention provides a method for determining whether a molecule affects the function or activity of an PKC pathway in a cell comprising: (a) contacting the cell with, or recombinantly expressing within a cell the molecule; and (b) determining whether the expression of one or more of the genes selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21) is changed relative to said expression in the absence of the molecule.

The invention provides a method for determining whether a molecule affects the function or activity of an *S. cerevisiae* Invasive Growth pathway in a cell comprising: (a) contacting the cell with, or recombinantly expressing within a cell the molecule; and (b) determining whether the expression of one or more of the genes selected from the group consisting of: KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29), is changed relative to said expression in the absence of the molecule.

5.2.1. CLUSTER ANALYSIS ALGORITHMS

Response profiles having been thus obtained and, optionally, screened to selected genes with significant responses, the genes and/or the individual response profiles are each grouped according to their similarities (FIG. 1, 103 and 104). In particular, the genes being analyzed according to the methods of the present invention are grouped or re-ordered into co-varying sets (FIG. 1, 103). Likewise, a similar grouping may be optionally performed to group the response profiles according to their similarity (FIG. 1, 104). The

steps of grouping the genes and grouping the response profiles may be performed in any order; *i.e.*, the genes may be grouped first. Preferably the genes and/or response profiles are each grouped by means of a pattern recognition procedure or algorithm, most preferably by means of a clustering procedure or algorithm. Such algorithms are well known to those of skill in the art, and are reviewed, *e.g.*, by Fukunaga, 1990, *Statistical Pattern Recognition*, 2nd Ed., London: Academic Press; Everitt, 1974, *Cluster Analysis*, London: Heinemann Educ. Books; Hartigan, 1975, *Clustering Algorithms*, New York: Wiley; Sneath & Sokal, 1973, *Numerical Taxonomy*, Freeman; and Anderberg, 1973, *Cluster Analysis for Applications*, New York: Academic Press, each of which is incorporated herein, by reference, in its entirety. Such algorithms include, for example, hierarchical agglomerative clustering algorithms, the "k-means" algorithm of Hartigan (*supra*), and model-based clustering algorithms such as *hclust* by MathSoft, Inc. In one preferred embodiment, the clustering analysis of the present invention is done using a hierarchical clustering algorithm, most preferably the *hclust* algorithm (see, *e.g.*, '*hclust*' routine from the software package S-Plus, MathSoft, Inc., Cambridge MA).

The clustering algorithms used in the present invention operate on tables of data containing gene expression measurements such as those described above. Specifically, the data tables analyzed by the clustering methods of the present invention comprise an $m \times k$ array or matrix wherein m is the total number of experimental conditions or perturbations and k is the number of genes measured and/or analyzed.

The clustering algorithms of the invention analyze such arrays or matrices to determine dissimilarities between the individual genes or between individual response profiles. For example, the dissimilarity between two genes i and j may be expressed mathematically as the "distance" $I_{i,j}$. A variety of distance metrics which are known to those skilled in the art which may be used in the clustering algorithms of the invention. For example, in one embodiment, the euclidian distance is determined according to the formula

$$I_{i,j} = \left[\sum_n \left(v_i^{(n)} - v_j^{(n)} \right)^2 \right]^{1/2} \quad (1)$$

wherein $v_i^{(n)}$ and $v_j^{(n)}$ are the response of genes i and j respectively to the perturbation n . In other embodiment, the Euclidian distance in Equation 1 above is squared to place progressively greater weight on cellular constituents that are further apart. In alternative embodiments, the distance measure I_{ij} is the Manhattan distance provided by

$$I_{i,j} = \sum_n |v_i^{(n)} - v_j^{(n)}| \quad (2)$$

In certain other embodiments the response profile data is categorical (*i.e.*, each the measured changes in gene expression is represented as either 1 or 0 in each profile), and the distance measure is preferably a percent disagreement defined by:

$$I_{i,j} = \frac{(\text{No. of } v_i^{(n)} \neq v_j^{(n)})}{N} \quad (3)$$

wherein N is the total number of response profiles.

In particularly preferred embodiments, the distance is defined as $I_{ij} = 1 - r_{ij}$, wherein r_{ij} is the "correlation coefficient" or normalized "dot product" between the genes i and j . In particular, r_{ij} is preferably defined by

$$r_{i,j} = \frac{v_i \cdot v_j}{|v_i||v_j|} \quad (4)$$

wherein the dot product $v_i \cdot v_j$ is provided by the expression

$$v_i \cdot v_j = \sum_n (v_i^{(n)} \times v_j^{(n)}) \quad (5)$$

and $|v_i| = (v_i \cdot v_i)^{1/2}$; $|v_j| = (v_j \cdot v_j)^{1/2}$.

In still other embodiments, the distance measure may be the Chebychev distance, the power distance, or the percent disagreement; all of which are well known in the art. Most preferably the distance measure is appropriate to the biological questions being asked, *i.e.*, for identifying co-regulated and/or co-varying genesets and, in particular, for identifying reporter genes and/or target genes within such genesets. Thus, in another particularly preferred embodiment, the correlation coefficient comprises a weighted dot product between genes i and j defined by the equation

$$r_{i,j} = \frac{\sum_n \frac{v_i^{(n)} v_j^{(n)}}{\sigma_i^{(n)} \sigma_j^{(n)}}}{\left[\sum_n \left(\frac{v_i^{(n)}}{\sigma_i^{(n)}} \right)^2 \sum_n \left(\frac{v_j^{(n)}}{\sigma_j^{(n)}} \right)^2 \right]^{1/2}} \quad (6)$$

wherein $\sigma_i^{(n)}$ and $\sigma_j^{(n)}$ are the standard errors associated with the measurement of genes i and j respectively in experiment n .

The correlation coefficients of Equations 4 and 6 are bonded between values of +1, which indicates that the two genes are perfectly correlated and essentially identical in

their response to perturbations, and -1, which indicates that the two genes are "anti-correlated" or "anti-sense" (*i.e.*, opposites). Thus, these correlation coefficients are particularly preferable in embodiments of the invention where the responses all have the same sign. However, in other embodiments it is preferable to identify genesets which are co-regulated or involved in the same biological response or pathways but which comprise similar and anti-correlated responses. In such embodiments, it is preferable to use the absolute value of Equation 4 or 6, *i.e.*, $|r_{ij}|$, as the correlation coefficient.

In still other embodiments, the relationships between co-regulated and/or co-varying genesets may be even more complex, such as in instances wherein multiple biological pathways (*e.g.*, signaling pathways) converge on the same cellular constituent to produce different outcomes. In such embodiments, it is preferable to use a correlation coefficient $r_{ij} = r_{ij}^{(change)}$ which is capable of identifying co-varying and/or co-regulated genes irrespective of the sign. The correlation specified by Equation 7 below is particularly useful in such embodiments.

$$r_{i,j}^{(change)} = \frac{\sum_n \left| \frac{v_i^{(n)}}{\sigma_i^{(n)}} \right| \left| \frac{v_j^{(n)}}{\sigma_j^{(n)}} \right|}{\left[\sum_n \left(\frac{v_i^{(n)}}{\sigma_i^{(n)}} \right)^2 \sum_n \left(\frac{v_j^{(n)}}{\sigma_j^{(n)}} \right)^2 \right]^{1/2}} \quad (7)$$

The cluster analysis methods may also be applied "two-dimensionally" in order to perform two-dimensional (2D) clustering analysis on the response profiles. Specifically, the clustering methods of the invention may be used both to cluster genes in co-varying genesets, and cluster response profiles into sets of similar response profiles, *i.e.*, perturbations that produce similar transcriptional responses. Such dual clustering is referred to herein as "two-dimensional clustering" or "two-dimensional cluster analysis". Distance metrics will be apparent to those skilled in the art for clustering the response profiles which are similar to those described above for clustering of genes. For example, one skilled in the art will readily appreciate that a suitable correlation coefficient $r^{(m,n)}$ for evaluating two response profiles m and n may be provided by a formula analogous to Equation 4 above:

$$r^{(m,n)} = \frac{v^{(n)} \cdot v^{(m)}}{|v^{(n)}| |v^{(m)}|} \quad (8)$$

wherein the dot product $v^{(n)} \cdot v^{(m)}$ is defined in a manner analogous to Equation 5 above, by the formula

$$v^{(n)} \cdot v^{(m)} = \sum_i (v_i^{(n)} \times v_i^{(m)}) \quad (9)$$

where $v_i^{(n)}$ and $v_i^{(m)}$ are the response of gene i to the perturbations n and m , respectively.

5 Generally, the clustering algorithms used in the methods of the invention also use one or more linkage rules to group cellular constituents into one or more sets or "clusters." For example, single linkage or the nearest neighbor method determines the distance between the two closest objects (*i.e.*, between the two closest genes) in a data table. By contrast, complete linkage methods determine the greatest distance between any two objects (*i.e.*, cellular constituents) in different clusters or sets. The unweighted pair-group
10 average evaluates the "distance" between two clusters or sets by determining the average distance between all pairs of objects (*i.e.*, genes) in the two clusters. Alternatively, the weighted pair-group average evaluates the distance between two clusters or sets by determining the weighted average distance between all pairs of objects in the two clusters, wherein the weighing factor is proportional to the size of the respective clusters. Other
15 linkage rules, such as the unweighted and weighted pair-group centroid and Ward's method, are also useful for certain embodiments of the present invention (see, *e.g.*, Ward, 1963, *J. Am. Stat. Assn.* 58:236; Hartigan, 1975, *Clustering Algorithms*, New York: Wiley; each of which is incorporated herein by reference in its entirety).

Once a clustering algorithm has grouped the genes from the data table into
20 sets or cluster (*i.e.*, into genesets) by application of linkage rules such as those described *supra*, a clustering "tree" may be generated to illustrate the genesets so determined. FIG. 14 illustrates an exemplary clustering tree generated by the *hclust* clustering algorithm upon analysis of a 34x185 table of response profile data using the distance metric $I_{ij} = 1 - r_{ij}$. The measured response data comprise the logarithm to the base 10 of the ratio between
25 abundances of each transcript in the pair conditions (*i.e.*, perturbation and no perturbation) comprising each experiment n .

Genesets may be readily defined based on the branchings of a clustering tree or diagram such as the one illustrated in FIG.14. In particular, genesets may be defined
30 based on the many smaller branchings of a clustering tree, or, optionally, larger genesets may be defined corresponding to the larger branches of a clustering tree. Preferably, the choice of branching level at which genesets are defined matches the number of distinct response pathways expected. In embodiments wherein little or no information is available to indicate the number of pathways, the genesets should be defined according to the branching level wherein the branches of the clustering tree are "truly distinct."

35 "Truly distinct," as used herein, is defined, *e.g.*, by a minimum distance value between the individual branches. Typically, the distance values between truly distinct

genesets are in the range of 0.2 to 0.4, where a distance of zero corresponds to perfect correlation and a distance of unity corresponds to no correlation. However, distances between truly distinct genesets may be larger in certain embodiments, *e.g.*, wherein there is poorer quality data or fewer experiments in the response profile data. Alternatively, in other
5 embodiments, *e.g.*, having better quality data or more experiments in the profile dataset, the distance between truly distinct genesets may be less than 0.2.

5.2.2. REPORTER GENES

Once genesets have been identified, *e.g.*, by means of the above-described
10 cluster analysis methods, reporter genes may be readily identified by anyone who is reasonably skilled in the art. In particular, any gene which clusters to a geneset associated with a particular biological effect or biological pathway is potentially useful as a reporter gene for that biological effect or biological pathway. Genesets associated with a particular biological effect or pathway can be readily identified, *e.g.*, by identifying other genes in the
15 geneset which are associated with the particular biological effect or pathway. Further, the members of a geneset associated with a particular biological effect or pathway will tend to be activated (or inhibited) by perturbations (*i.e.*, in response profiles) which target a particular biological effect or pathway. Thus, geneset associated with a particular biological effect or pathway can also be identified by identifying genesets that respond (*i.e.*, whose
20 members are activated or inhibited) to perturbations that target the particular biological effect or pathway.

Preferably, the reporter genes of the invention also have one or more of the following characteristics. First, the reporter genes of the invention should be highly specific for the biological effect or pathway of interest. In particular, the reporter genes of the
25 present invention should cluster specifically to genesets associated with the biological effect or pathway of interest, and their expression should not be altered, or, less preferably, should only be slightly altered, by perturbations which target other biological effects or pathways.

Second, the reporter genes of the invention preferably have a high level of induction. In particular, the reporter genes of the invention are preferably expressed at high
30 levels, and their level of expression changes significantly in response to perturbations of the biological effect or pathway of interest. For example, in one embodiment, expression of a reporter genes of the invention changes at least two fold in response to a perturbation to the biological effect or pathway of interest. In a more preferred embodiment, expression of a reporter gene of the invention changes by at least ten fold in response to a perturbation to
35 the biological effect or pathway of interest. Most preferably, a reporter gene of the

invention will change by a factor of one hundred or more in response to a perturbation to the biological effect or pathway of interest.

The reporter genes of the invention are also preferably sensitive to perturbations to the biological effect or pathway of interest. In particular, preferably the reporter genes of the invention are perturbed (*i.e.*, their expression is up-regulated or down-regulated) at measurable levels in response to only slight perturbations to the biological effect or pathway of interest, such as in response to low doses of a drug which targets the biological effect or pathway of interest. More preferably, the reporter genes of the invention are more sensitive to perturbations to the biological effect or pathway of interest than are other genes in the geneset for that biological effect or pathway.

In most embodiments, the reporter genes of the invention are preferably general reporters for the entire biological effect or pathway of interest. More specifically, the reporter genes preferably cluster, and therefore respond, to perturbations targeted to the entire biological effect or pathway of interest and not just to particular portions thereof (*e.g.*, to early or late steps of a particular biological pathway). However, one skill of the art can readily appreciate that in certain embodiments it will be useful to identify reporter genes for a particular part of a biological effect or pathway of interest. Accordingly, in such embodiments, the reporter genes identified are preferably specific for those particular portions of the biological effect or pathway that are of interest.

Finally, in certain embodiments, the reporter genes of the invention are genes which kinetically induce quickly, and therefore respond quickly to perturbations of the biological effect or pathway of interest. For example, in most embodiments, changes in the reporter genes of the invention will preferably reach steady state within about eight hours after a perturbation (*e.g.*, after exposure to a drug which targets a biological effect or pathway of interest). More preferably, a reporter gene of the invention induces within about six hours after a perturbation. In other preferred embodiments, a reporter gene of the invention induces within about 2 hours, within about ninety minutes, within about sixty minutes, within about thirty minutes, within about ten minutes, or within about seven minutes after a perturbation.

Other embodiments of the invention provides methods for using combinations of genes to construct a more specific reporter for a particular biological pathway in which it is desired to increase the specificity of a particular pathway reporter system. In this embodiment, more than one gene, or cellular constituent in the same biological pathway is used as a reporter for that pathway. By way of example, a reporter gene of the Invasive Growth pathway such as PGU1, and a second gene in the same pathway such as SVS1, may be detected simultaneously as a reporter for the Invasive

Growth pathway. Such co-detection can serve to increase the sensitivity of a reporter of a particular biological pathway. Alternatively, for example, the promoter from a first gene of the Invasive Growth pathway, such as PGU1 may be fused to a marker such as GFP (green fluorescent protein), and a the promoter from a second gene in the same pathway such as SVS1, could be fused to BFP (blue fluorescent protein). Detection of the both proteins makers simultaneuosly can thus provides a higher sensitivity. Thus in this embodiment, the reporter of the pathway is a combination of two or more genes. In other embodiment of the invention, a 2-3, 3-5, 5-10 genes are detected simultaneously as a reporter system for a particular biological pathway.

10 The invention provides a method of identifying a reporter gene for a particular biological pathway in a cell comprising identifying a gene which clusters to a geneset associated with the biological pathway, wherein said gene which clusters to the geneset associated with the particular biological pathway is a reporter gene.

In one embodiment the reporter gene is a reporter for the ergosterol-pathway, and the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9).

20 In another embodiment the reporter gene is a reporter for the PKC-pathway, and the reporter gene is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21).

In another embodiment the reporter gene is a reporter for the Invasive Growth pathway, and the reporter gene selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

5.2.3. TARGET GENES

35 Once genesets have been identified, e.g., by means of the above-described cluster analysis methods, target genes may be readily identified in the following manner.

Any gene which clusters to a geneset associated with a particular biological effect or biological pathway may be considered a potential target gene and may further be tested to examine whether the expression and/or activity of the gene is necessary for normal activity or function of the pathway. A gene whose expression and/or activity is necessary for normal activity or function of the pathway is therefore useful as a target for drugs designed to enhance, inhibit, or modulate the particular biological pathway. Any method known in the art may be used to examine the necessity of a particular gene to the activity or function of an associated biological pathway. For example, by way of illustration, potential target gene, such as a potential ergosterol-pathway target gene may be validated as a target gene in the following manner.

Once a potential target gene has been identified (e.g., by clustering analysis as described herein), the gene may be examined by mutational analysis to determine whether the gene is essential. Methods for mutational analysis are commonly known in the art. If the potential ergosterol-pathway target gene is essential for normal growth of the yeast, such a gene is a target gene. Such a gene would constitute a preferred target for antifungal or fungicidal drug development. Further, additional genetic analysis may be performed in order to construct and characterize a conditional allele of the gene in order to determine the effects of gene product inhibition, particularly whether the cell dies upon shifting to the restrictive condition, or whether the cell can recover upon shifting back to the permissive condition. Any method known in the art may be used to construct a conditional allele, for example, a temperature sensitive allele, or promoter replacement may be performed so that expression may be regulated. The construction of a conditional allele also allows for the determination of the terminal phenotype, contributing to an understanding of the function of the gene. If, for example, the potential ergosterol-pathway gene is determined not to be essential in *S. cerevisiae*, or if a severe growth defect does not result from deletion of the gene, the gene is not a preferred target gene for the development of a pathway-specific drug such as an antifungal agent.

Another way in which a potential target gene may be validated is by searching the sequence database for a homolog genes. For example, in the case of an *S. cerevisiae* target gene, a database from the yeast *Candida* may serve as a database for which to compare sequence. Alternatively, a search of all sequence databases may be performed to uncover sequence motifs that will reveal potential activities of the gene. Specifically, by way of example computer programs for determining homology include but are not limited to TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, Proc. Natl. Acad. Sci. USA 85(8):2444-8; Altschul et al., 1990, J. Mol. Biol. 215(3):403-10; Thompson, et al., 1994, Nucleic Acids Res. 22(22):4673-80; Higgins, et al., 1996, Methods

Enzymol 266:383-402; Altschul, et al., 1990, J. Mol. Biol. 215(3):403-10). If, for example, a homolog of the *S. cerevisiae* target gene is found in *Candida*, the *Candida* gene may be analyzed as above to determine whether the homolog is essential in *Candida*, and would constitute a validated target.

- 5 The invention provides a method of identifying a target gene for a particular biological pathway in a cell comprising identifying a gene which clusters to a geneset associated with the particular biological pathway, wherein said gene which clusters to a geneset associated with the particular biological pathway and is identified as a gene which is necessary for normal function of said particular biological pathway.

10

5.3. PERTURBATION METHODS

- Methods for perturbation of biological pathways at various levels of a cell are increasingly widely known and applied in the art. Any such methods that are capable of specifically targeting and controllably modifying (e.g., either by a graded increase or
15 activation or by a graded decrease or inhibition) specific cellular constituents (e.g., gene expression, RNA concentrations, protein abundances, protein activities, or so forth) can be employed in performing pathway perturbations. Controllable modifications of cellular constituents consequentially controllably perturb pathways originating at the modified cellular constituents. Such pathways originating at specific cellular constituents are
20 preferably employed to represent drug action in this invention. Preferable modification methods are capable of individually targeting each of a plurality of cellular constituents and most preferably a substantial fraction of such cellular constituents.

- The following methods are exemplary of those that can be used to modify cellular constituents and thereby to produce pathway perturbations which generate the
25 pathway responses used in the steps of the methods of this invention as previously described. This invention is adaptable to other methods for making controllable perturbations to pathways, and especially to cellular constituents from which pathways originate.

- Pathway perturbations are preferably made in cells of cell types derived from
30 any organism for which genomic or expressed sequence information is available and for which methods are available that permit controllably modification of the expression of specific genes. Genome sequencing is currently underway for several eukaryotic organisms, including humans, nematodes, *Arabidopsis*, and flies. In a preferred embodiment, the invention is carried out using a yeast, with *Saccharomyces cerevisiae* most
35 preferred because the sequence of the entire genome of a *S. cerevisiae* strain has been determined. In addition, well-established methods are available for controllably modifying

expression of year genes. A preferred strain of yeast is a *S. cerevisiae* strain for which yeast genomic sequence is known, such as strain S288C or substantially isogenic derivatives of it (see, e.g., Dujon *et al.*, 1994, *Nature* 369:371-378; Bussey *et al.*, 1995, *Proc. Natl. Acad. Sci. U.S.A.* 92:3809-3813; Feldmann *et al.*, 1994, *E.M.B.O. J.* 13:5795-5809; Johnston *et al.*, 1994, *Science* 265:2077-2082; Galibert *et al.*, 1996, *E.M.B.O. J.* 15:2031-2049).
5 However, other strains may be used as well. Yeast strains are available, e.g., from American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209. Standard techniques for manipulating yeast are described in C. Kaiser, S. Michaelis, & A. Mitchell, 1994, *Methods in Yeast Genetics: A Cold Spring Harbor*
10 *Laboratory Course Manual*, Cold Spring Harbor Laboratory Press, New York; and Sherman *et al.*, 1986, *Methods in Yeast Genetics: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor. New York.

The exemplary methods described in the following include use of titratable expression systems, use of transfection or viral transduction systems, direct modifications to
15 RNA abundances or activities, direct modifications of protein abundances, and direct modification of protein activities including use of drugs (or chemical moieties in general) with specific known action.

5.3.1. TITRATABLE EXPRESSION SYSTEMS

20 Any of the several known titratable, or equivalently controllable, expression systems available for use in the budding yeast *Saccharomyces cerevisiae* are adaptable to this invention (Mumberg *et al.*, 1994, *Nucl. Acids Res.* 22:5767-5768). Usually, gene expression is controlled by transcriptional controls, with the promoter of the gene to be controlled replaced on its chromosome by a controllable, exogenous promoter. The most
25 commonly used controllable promoter in yeast is the GAL1 promoter (Johnston *et al.*, 1984, *Mol Cell. Biol.* 8:1440-1448). The GAL1 promoter is strongly repressed by the presence of glucose in the growth medium, and is gradually switched on in a graded manner to high levels of expression by the decreasing abundance of glucose and the presence of galactose. The GAL1 promoter usually allows a 5-100 fold range of expression control on a gene of
30 interest.

Other frequently used promoter systems include the MET25 promoter (Kerjan *et al.*, 1986, *Nucl. Acids. Res.* 14:7861-7871), which is induced by the absence of methionine in the growth medium, and the CUP1 promoter, which is induced by copper (Mascorro-Gallardo *et al.*, 1996, *Gene* 172:169-170). All of these promoter systems are
35 controllable in that gene expression can be incrementally controlled by incremental changes in the abundances of a controlling moiety in the growth medium.

One disadvantage of the above listed expression systems is that control of promoter activity (effected by, e.g., changes in carbon source, removal of certain amino acids), often causes other changes in cellular physiology which independently alter the expression levels of other genes. A recently developed system for yeast, the Tet system, alleviates this problem to a large extent (Gari et al., 1997, *Yeast* 13:837-848). The Tet promoter, adopted from mammalian expression systems (Gossen et al., 1995, *Proc. Nat. Acad. Sci. USA* 89:5547-5551) is modulated by the concentration of the antibiotic tetracycline or the structurally related compound doxycycline. Thus, in the absence of doxycycline, the promoter induces a high level of expression, and the addition of increasing levels of doxycycline causes increased repression of promoter activity. Intermediate levels of gene expression can be achieved in the steady state by addition of intermediate levels of drug. Furthermore, levels of doxycycline that give maximal repression of promoter activity (10 micrograms/ml) have no significant effect on the growth rate on wild type yeast cells (Gari et al., 1997, *Yeast* 13:837-848).

In mammalian cells, several means of titrating expression of genes are available (Spencer, 1996, *Trends Genet.* 12:181-187). As mentioned above, the Tet system is widely used, both in its original form, the "forward" system, in which addition of doxycycline represses transcription, and in the newer "reverse" system, in which doxycycline addition stimulates transcription (Gossen et al., 1995, *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Hoffmann et al., 1997, *Nucl. Acids. Res.* 25:1078-1079; Hofmann et al., 1996, *Proc. Natl. Acad. Sci. USA* 83:5185-5190; Paulus et al., 1996, *Journal of Virology* 70:62-67). Another commonly used controllable promoter system in mammalian cells is the ecdysone-inducible system developed by Evans and colleagues (No et al., 1996, *Proc. Nat. Acad. Sci. USA* 93:3346-3351), where expression is controlled by the level of muristerone added to the cultured cells. Finally, expression can be modulated using the "chemical-induced dimerization" (CID) system developed by Schreiber, Crabtree, and colleagues (Belshaw et al., 1996, *Proc. Nat. Acad. Sci. USA* 93:4604-4607; Spencer, 1996, *Trends Genet.* 12:181-187) and similar systems in yeast. In this system, the gene of interest is put under the control of the CID-responsive promoter, and transfected into cells expressing two different hybrid proteins, one comprised of a DNA-binding domain fused to FKBP12, which binds FK506. The other hybrid protein contains a transcriptional activation domain also fused to FKBP12. The CID inducing molecule is FK1012, a homodimeric version of FK506 that is able to bind simultaneously both the DNA binding and transcriptional activating hybrid proteins. In the graded presence of FK1012, graded transcription of the controlled gene is activated.

For each of the mammalian expression systems described above, as is widely known to those of skill in the art, the gene of interest is put under the control of the controllable promoter, and a plasmid harboring this construct along with an antibiotic resistance gene is transfected into cultured mammalian cells. In general, the plasmid DNA
5 integrates into the genome, and drug resistant colonies are selected and screened for appropriate expression of the regulated gene. Alternatively, the regulated gene can be inserted into an episomal plasmid such as pCEP4 (Invitrogen, Inc.), which contains components of the Epstein-Barr virus necessary for plasmid replication.

In a preferred embodiment, titratable expression systems, such as the ones
10 described above, are introduced for use into cells or organisms lacking the corresponding endogenous gene and/or gene activity, *e.g.*, organisms in which the endogenous gene has been disrupted or deleted. Methods for producing such "knock outs" are well known to those of skill in the art, see *e.g.*, Pettitt *et al.*, 1996, *Development* 122:4149-4157; Spradling
15 *et al.*, 1995, *Proc. Natl. Acad. Sci. USA*, 92:10824-10830; Ramirez-Solis *et al.*, 1993, *Methods Enzymol.* 225:855-878; and Thomas *et al.*, 1987, *Cell* 51:503-512.

5.3.2. TRANSFECTION SYSTEMS FOR MAMMALIAN CELLS

Transfection or viral transduction of target genes can introduce controllable perturbations in biological pathways in mammalian cells. Preferably, transfection or
20 transduction of a target gene can be used with cells that do not naturally express the target gene of interest. Such non-expressing cells can be derived from a tissue not normally expressing the target gene or the target gene can be specifically mutated in the cell. The target gene of interest can be cloned into one of many mammalian expression plasmids, for example, the pcDNA3.1 +/- system (Invitrogen, Inc.) or retroviral vectors, and introduced
25 into the non-expressing host cells. Transfected or transduced cells expressing the target gene may be isolated by selection for a drug resistance marker encoded by the expression vector. The level of gene transcription is monotonically related to the transfection dosage. In this way, the effects of varying levels of the target gene may be investigated.

A particular example of the use of this method is the search for drugs that
30 target the src-family protein tyrosine kinase, lck, a key component of the T cell receptor activation pathway (Anderson *et al.*, 1994, *Adv. Immunol.* 56:171-178). Inhibitors of this enzyme are of interest as potential immunosuppressive drugs (Hanke JH, 1996, *J. Biol Chem* 271(2):695-701). A specific mutant of the Jurkat T cell line (JCaM1) is available that does not express lck kinase (Straus *et al.*, 1992, *Cell* 70:585-593). Therefore, introduction
35 of the lck gene into JCaM1 by transfection or transduction permits specific perturbation of pathways of T cell activation regulated by the lck kinase. The efficiency of transfection or

transduction, and thus the level of perturbation, is dose related. The method is generally useful for providing perturbations of gene expression or protein abundances in cells not normally expressing the genes to be perturbed.

5 5.3.3. METHODS OF MODIFYING RNA ABUNDANCES OR ACTIVITIES

Methods of modifying RNA abundances and activities currently fall within three classes, ribozymes, antisense species, and RNA aptamers (Good *et al.*, 1997, *Gene Therapy* 4: 45-54). Controllable application or exposure of a cell to these entities permits
10 controllable perturbation of RNA abundances.

Ribozymes are RNAs which are capable of catalyzing RNA cleavage reactions. (Cech, 1987, *Science* 236:1532-1539; PCT International Publication WO 90/11364, published October 4, 1990; Sarver *et al.*, 1990, *Science* 247: 1222-1225). "Hairpin" and "hammerhead" RNA ribozymes can be designed to specifically cleave a
15 particular target mRNA. Rules have been established for the design of short RNA molecules with ribozyme activity, which are capable of cleaving other RNA molecules in a highly sequence specific way and can be targeted to virtually all kinds of RNA. (Haseloff *et al.*, 1988, *Nature* 334:585-591; Koizumi *et al.*, 1988, *FEBS Lett.* 228:228-230; Koizumi *et al.*, 1988, *FEBS Lett.* 239:285-288). Ribozyme methods involve exposing a cell to,
20 inducing expression in a cell, etc. of such small RNA ribozyme molecules. (Grassi and Marini, 1996, *Annals of Medicine* 28: 499-510; Gibson, 1996, *Cancer and Metastasis Reviews* 15: 287-299).

Ribozymes can be routinely expressed *in vivo* in sufficient number to be catalytically effective in cleaving mRNA, and thereby modifying mRNA abundances in a
25 cell. (Cotten *et al.*, 1989, *EMBO J.* 8:3861-3866). In particular, a ribozyme coding DNA sequence, designed according to the previous rules and synthesized, for example, by standard phosphoramidite chemistry, can be ligated into a restriction enzyme site in the anticodon stem and loop of a gene encoding a tRNA, which can then be transformed into and expressed in a cell of interest by methods routine in the art. Preferably, an inducible
30 promoter (*e.g.*, a glucocorticoid or a tetracycline response element) is also introduced into this construct so that ribozyme expression can be selectively controlled. tDNA genes (*i.e.*, genes encoding tRNAs) are useful in this application because of their small size, high rate of transcription, and ubiquitous expression in different kinds of tissues. Therefore, ribozymes can be routinely designed to cleave virtually any mRNA sequence, and a cell can
35 be routinely transformed with DNA coding for such ribozyme sequences such that a controllable and catalytically effective amount of the ribozyme is expressed. Accordingly the abundance of virtually any RNA species in a cell can be perturbed.

In another embodiment, activity of a target RNA (preferable mRNA) species, specifically its rate of translation, can be controllably inhibited by the controllable application of antisense nucleic acids. An "antisense" nucleic acid as used herein refers to a nucleic acid capable of hybridizing to a sequence-specific (e.g., non-poly A) portion of the target RNA, for example its translation initiation region, by virtue of some sequence complementarity to a coding and/or non-coding region. The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA or a modification or derivative thereof, which can be directly administered in a controllable manner to a cell or which can be produced intracellularly by transcription of exogenous, introduced sequences in controllable quantities sufficient to perturb translation of the target RNA.

Preferably, antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides (ranging from 6 to about 200 oligonucleotides). In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, or agents facilitating transport across the cell membrane (see, e.g., Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci. U.S.A.* 84: 648-652; PCT Publication No. WO 88/09810, published December 15, 1988), hybridization-triggered cleavage agents (see, e.g., Krol *et al.*, 1988, *BioTechniques* 6: 958-976) or intercalating agents (see, e.g., Zon, 1988, *Pharm. Res.* 5: 539-549).

In a preferred aspect of the invention, an antisense oligonucleotide is provided, preferably as single-stranded DNA. The oligonucleotide may be modified at any position on its structure with constituents generally known in the art.

The antisense oligonucleotides may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine,

2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

In another embodiment, the oligonucleotide comprises at least one modified
5 sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a
10 methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the oligonucleotide is a 2- α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier *et al.*, 1987, *Nucl. Acids Res.* 15: 6625-6641).

15 The oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of a target RNA species. However, absolute
20 complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both
25 the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with a target RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex. The amount of antisense nucleic acid that will be
30 effective in the inhibiting translation of the target RNA can be determined by standard assay techniques.

Oligonucleotides of the invention may be synthesized by standard methods known in the art, *e.g.* by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate
35 oligonucleotides may be synthesized by the method of Stein *et al.* (1988, *Nucl. Acids Res.* 16: 3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore

glass polymer supports (Sarin *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85: 7448-7451), etc. In another embodiment, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, 1987, *Nucl. Acids Res.* 15: 6131-6148), or a chimeric RNA-DNA analog (Inoue *et al.*, 1987, *FEBS Lett.* 215: 327-330).

5 The synthesized antisense oligonucleotides can then be administered to a cell in a controlled manner. For example, the antisense oligonucleotides can be placed in the growth environment of the cell at controlled levels where they may be taken up by the cell. The uptake of the antisense oligonucleotides can be assisted by use of methods well known in the art.

10 In an alternative embodiment, the antisense nucleic acids of the invention are controllably expressed intracellularly by transcription from an exogenous sequence. For example, a vector can be introduced *in vivo* such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the antisense nucleic
15 acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequences encoding the antisense RNAs can be by any promoter known
20 in the art to act in a cell of interest. Such promoters can be inducible or constitutive. Most preferably, promoters are controllable or inducible by the administration of an exogenous moiety in order to achieve controlled expression of the antisense oligonucleotide. Such controllable promoters include the Tet promoter. Less preferably usable promoters for mammalian cells include, but are not limited to: the SV40 early promoter region (Bernoist
25 and Chambon, 1981, *Nature* 290: 304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, *Cell* 22: 787-797), the herpes thymidine kinase promoter (Wagner *et al.*, 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78: 1441-1445), the regulatory sequences of the metallothionein gene (Brinster *et al.*, 1982, *Nature* 296: 39-42), etc.

30 Therefore, antisense nucleic acids can be routinely designed to target virtually any mRNA sequence, and a cell can be routinely transformed with or exposed to nucleic acids coding for such antisense sequences such that an effective and controllable amount of the antisense nucleic acid is expressed. Accordingly the translation of virtually any RNA species in a cell can be controllably perturbed.

35 Finally, in a further embodiment, RNA aptamers can be introduced into or expressed in a cell. RNA aptamers are specific RNA ligands for proteins, such as for Tat

and Rev RNA (Good *et al.*, 1997, *Gene Therapy* 4: 45-54) that can specifically inhibit their translation.

In specific embodiments of the invention methods of modifying RNA abundances and activities are used to modify an RNA corresponding to a target gene or reporter gene of the invention. In other specific embodiments of the invention, a ribozymes, antisense species, and RNA aptamers directed to a target gene of the invention is used as a drug or therapeutic agent.

5.3.4. METHODS OF MODIFYING PROTEIN ABUNDANCES

Methods of modifying protein abundances include, *inter alia*, those altering protein degradation rates and those using antibodies (which bind to proteins affecting abundances of activities of native target protein species). Increasing (or decreasing) the degradation rates of a protein species decreases (or increases) the abundance of that species. Methods for controllably increasing the degradation rate of a target protein in response to elevated temperature and/or exposure to a particular drug, which are known in the art, can be employed in this invention. For example, one such method employs a heat-inducible or drug-inducible N-terminal degron, which is an N-terminal protein fragment that exposes a degradation signal promoting rapid protein degradation at a higher temperature (*e.g.*, 37° C) and which is hidden to prevent rapid degradation at a lower temperature (*e.g.*, 23° C) (Dohmen *et al.*, 1994, *Science* 263:1273-1276). Such an exemplary degron is Arg-DHFR^{ts}, a variant of murine dihydrofolate reductase in which the N-terminal Val is replaced by Arg and the Pro at position 66 is replaced with Leu. According to this method, for example, a gene for a target protein, P, is replaced by standard gene targeting methods known in the art (Lodish *et al.*, 1995, *Molecular Biology of the Cell*, Chpt. 8, New York: W.H. Freeman and Co.) with a gene coding for the fusion protein Ub-Arg-DHFR^{ts}-P ("Ub" stands for ubiquitin). The N-terminal ubiquitin is rapidly cleaved after translation exposing the N-terminal degron. At lower temperatures, lysines internal to Arg-DHFR^{ts} are not exposed, ubiquitination of the fusion protein does not occur, degradation is slow, and active target protein levels are high. At higher temperatures (in the absence of methotrexate), lysines internal to Arg-DHFR^{ts} are exposed, ubiquitination of the fusion protein occurs, degradation is rapid, and active target protein levels are low. Heat activation of degradation is controllably blocked by exposure methotrexate. This method is adaptable to other N-terminal degrons which are responsive to other inducing factors, such as drugs and temperature changes.

Target protein abundances and also, directly or indirectly, their activities can also be decreased by (neutralizing) antibodies. By providing for controlled exposure to

such antibodies, protein abundances/activities can be controllably modified. For example, antibodies to suitable epitopes on protein surfaces may decrease the abundance, and thereby indirectly decrease the activity, of the wild-type active form of a target protein by aggregating active forms into complexes with less or minimal activity as compared to the wild-type unaggregated wild-type form. Alternately, antibodies may directly decrease protein activity by, *e.g.*, interacting directly with active sites or by blocking access of substrates to active sites. Conversely, in certain cases, (activating) antibodies may also interact with proteins and their active sites to increase resulting activity. In either case, antibodies (of the various types to be described) can be raised against specific protein species (by the methods to be described) and their effects screened. The effects of the antibodies can be assayed and suitable antibodies selected that raise or lower the target protein species concentration and/or activity. Such assays involve introducing antibodies into a cell (see below), and assaying the concentration of the wild-type amount or activities of the target protein by standard means (such as immunoassays) known in the art. The net activity of the wild-type form can be assayed by assay means appropriate to the known activity of the target protein.

Antibodies can be introduced into cells in numerous fashions, including, for example, microinjection of antibodies into a cell (Morgan *et al.*, 1988, *Immunology Today* 9:84-86) or transforming hybridoma mRNA encoding a desired antibody into a cell (Burke *et al.*, 1984, *Cell* 36:847-858). In a further technique, recombinant antibodies can be engineering and ectopically expressed in a wide variety of non-lymphoid cell types to bind to target proteins as well as to block target protein activities (Biocca *et al.*, 1995, *Trends in Cell Biology* 5:248-252). Preferably, expression of the antibody is under control of a controllable promoter, such as the Tet promoter. A first step is the selection of a particular monoclonal antibody with appropriate specificity to the target protein (see below). Then sequences encoding the variable regions of the selected antibody can be cloned into various engineered antibody formats, including, for example, whole antibody, Fab fragments, Fv fragments, single chain Fv fragments (V_H and V_L regions united by a peptide linker) ("ScFv" fragments), diabodies (two associated ScFv fragments with different specificities), and so forth (Hayden *et al.*, 1997, *Current Opinion in Immunology* 9:210-212). Intracellularly expressed antibodies of the various formats can be targeted into cellular compartments (*e.g.*, the cytoplasm, the nucleus, the mitochondria, etc.) by expressing them as fusions with the various known intracellular leader sequences (Bradbury *et al.*, 1995, *Antibody Engineering*, vol. 2, Borrebaeck ed., IRL Press, pp 295-361). In particular, the ScFv format appears to be particularly suitable for cytoplasmic targeting.

Antibody types include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library. Various procedures known in the art may be used for the production of polyclonal antibodies to a target protein. For production of the antibody, various host animals can be immunized by injection with the target protein, such host animals include, but are not limited to, rabbits, mice, rats, etc. Various adjuvants can be used to increase the immunological response, depending on the host species, and include, but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, and potentially useful human adjuvants such as bacillus Calmette-Guerin (BCG) and corynebacterium parvum.

For preparation of monoclonal antibodies directed towards a target protein, any technique that provides for the production of antibody molecules by continuous cell lines in culture may be used. Such techniques include, but are not restricted to, the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature* 256: 495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, 1983, *Immunology Today* 4: 72), and the EBV hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing recent technology (PCT/US90/02545). According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80: 2026-2030), or by transforming human B cells with EBV virus *in vitro* (Cole *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison *et al.*, 1984, *Proc. Natl. Acad. Sci. U.S.A.* 81: 6851-6855; Neuberger *et al.*, 1984, *Nature* 312:604-608; Takeda *et al.*, 1985, *Nature* 314: 452-454) by splicing the genes from a mouse antibody molecule specific for the target protein together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention.

Additionally, where monoclonal antibodies are advantageous, they can be alternatively selected from large antibody libraries using the techniques of phage display (Marks *et al.*, 1992, *J. Biol. Chem.* 267:16007-16010). Using this technique, libraries of up to 10^{12} different antibodies have been expressed on the surface of fd filamentous phage, creating a "single pot" *in vitro* immune system of antibodies available for the selection of monoclonal antibodies (Griffiths *et al.*, 1994, *EMBO J.* 13:3245-3260). Selection of antibodies from such libraries can be done by techniques known in the art, including

contacting the phage to immobilized target protein, selecting and cloning phage bound to the target, and subcloning the sequences encoding the antibody variable regions into an appropriate vector expressing a desired antibody format.

According to the invention, techniques described for the production of single chain antibodies (U.S. patent 4,946,778) can be adapted to produce single chain antibodies specific to the target protein. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse *et al.*, 1989, *Science* 246: 1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for the target protein.

Antibody fragments that contain the idiotypes of the target protein can be generated by techniques known in the art. For example, such fragments include, but are not limited to: the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments that can be generated by reducing the disulfide bridges of the F(ab')₂ fragment, the Fab fragments that can be generated by treating the antibody molecule with papain and a reducing agent, and Fv fragments.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, *e.g.*, ELISA (enzyme-linked immunosorbent assay). To select antibodies specific to a target protein, one may assay generated hybridomas or a phage display antibody library for an antibody that binds to the target protein.

5.3.5. METHODS OF MODIFYING PROTEIN ACTIVITIES

Methods of directly modifying protein activities include, *inter alia*, dominant negative mutations, specific drugs (used in the sense of this application) or chemical moieties generally, and also the use of antibodies, as previously discussed.

Dominant negative mutations are mutations to endogenous genes or mutant exogenous genes that when expressed in a cell disrupt the activity of a targeted protein species. Depending on the structure and activity of the targeted protein, general rules exist that guide the selection of an appropriate strategy for constructing dominant negative mutations that disrupt activity of that target (Hershkowitz, 1987, *Nature* 329:219-222). In the case of active monomeric forms, over expression of an inactive form can cause competition for natural substrates or ligands sufficient to significantly reduce net activity of the target protein. Such over expression can be achieved by, for example, associating a promoter, preferably a controllable or inducible promoter, of increased activity with the mutant gene. Alternatively, changes to active site residues can be made so that a virtually irreversible association occurs with the target ligand. Such can be achieved with certain

tyrosine kinases by careful replacement of active site serine residues (Perlmutter *et al.*, 1996, *Current Opinion in Immunology* 8:285-290).

In the case of active multimeric forms, several strategies can guide selection of a dominant negative mutant. Multimeric activity can be controllably decreased by
5 expression of genes coding exogenous protein fragments that bind to multimeric association domains and prevent multimer formation. Alternatively, controllable over expression of an inactive protein unit of a particular type can tie up wild-type active units in inactive multimers, and thereby decrease multimeric activity (Nocka *et al.*, 1990, *EMBO J.* 9:1805-1813). For example, in the case of dimeric DNA binding proteins, the DNA binding
10 domain can be deleted from the DNA binding unit, or the activation domain deleted from the activation unit. Also, in this case, the DNA binding domain unit can be expressed without the domain causing association with the activation unit. Thereby, DNA binding sites are tied up without any possible activation of expression. In the case where a particular type of unit normally undergoes a conformational change during activity,
15 expression of a rigid unit can inactivate resultant complexes. For a further example, proteins involved in cellular mechanisms, such as cellular motility, the mitotic process, cellular architecture, and so forth, are typically composed of associations of many subunits of a few types. These structures are often highly sensitive to disruption by inclusion of a few monomeric units with structural defects. Such mutant monomers disrupt the relevant
20 protein activities and can be controllably expressed in a cell.

In addition to dominant negative mutations, mutant target proteins that are sensitive to temperature (or other exogenous factors) can be found by mutagenesis and screening procedures that are well-known in the art.

Also, one of skill in the art will appreciate that expression of antibodies
25 binding and inhibiting a target protein can be employed as another dominant negative strategy.

5.3.6. DRUGS OF SPECIFIC KNOWN ACTION

Additionally, activities of certain proteins can be controllably altered by
30 exposure to exogenous drugs or ligands. In a preferable case, a drug is known that interacts with only one target protein in the cell and alters the activity of only that one target protein. Graded exposure of a cell to varying amounts of that drug thereby causes graded perturbations of pathways originating at that protein. The alteration can be either a decrease or an increase of activity. Less preferably, a drug is known and used that alters the activity
35 of only a few (*e.g.*, 2-5) target proteins with separate, distinguishable, and non-overlapping

effects. Graded exposure to such a drug causes graded perturbations to the several pathways originating at the target proteins.

In a specific embodiment of the invention, when the pathway of interest is the yeast ergosterol-pathway, a known drug which acts as an inhibitor of ergosterol-biosynthesis may be used to perturb the pathway. Ergosterol is the primary membrane sterol in fungi and in some trypanosomes. Ergosterol serves a structural role comparable to that of cholesterol in mammalian cells, and is essential for the integrity and structure of the fungal cell membrane. As depicted in Figure 12, the ergosterol synthesis pathway contains at least 18 genes designated ERG1 through EGR26. Several different classes of antifungal agents exist which target the ergosterol-pathway. Such drugs or agents may be used in connection with the methods of the invention. In one embodiment, the a known antifungal drug is used to perturb the ergosterol-pathway. Such drugs include but are not limited to the following.

The polyenes are a class of drugs that bind to ergosterol in the fungal membrane, causing the cells to become leaky and die (Hamilton-Miller, J., 1973, Bacteriol. Rev. 37:166). Polyenes and derivatives, include drugs such as amphotericin B, nystatin, and pimaricin.

Azoles are a second class of drug which target the ergosterol-pathway. Azoles act to inhibit C-14 demethylation of an ergosterol precursor called lanosterol. Normally in the synthesis of the ergosterol, the EGR11 gene product acts to demethylate C-14 of lanosterol. Azoles inhibit this process leading to a C-14 methylsterol product. Consequently, incorporation of these altered products into the fungal membrane in place of ergosterol, leads to reduced membrane fluidity, reduced fungal growth, and reduced invasiveness. Azoles, include drugs such as clotrimazole, intraconazole, fluconazole, miconazole, econazole, sulconazole, and ketoconazole.

A third class of ergosterol-pathway drug are the allylamines-thiocarbamates which act to inhibit squalene epoxidase, the ERG1 gene product. Allylamines-thiocarbamates derivatives include naftifine, tolnaftate, and terbinafine.

The morpholines are a forth class of drug that affect ergosterol synthesis. Morpholines, such as amorolfine, act to block two separate steps of the ergosterol synthesis pathway. Morpholines inhibit C-14 sterol reduction by the ERG24 gene product. Morpholines also inhibit isomerization of sterol $\Delta 8 \rightarrow 7$ by the ERG2 gene product.

As will be appreciated by one skilled in the art, any known drug associated with a particular biological pathway of interest may be used in connection with the methods of the invention, for example, as an agent to perturb the particular biological pathway.

5.4. PREPARING THE MICROARRAY

The invention herein provides methods of using microarray technology to identify reporter genes and target genes of a particular biological pathway. Microarray may be prepared by any method known in the art, including but not limited to the preparation methods described herein below.

5.4.1. BINDING SITES ON THE MICROARRAYS

As noted above, the "binding site" to which a particular polynucleotide molecule specifically hybridizes according to the invention is usually a complementary polynucleotide sequence. In one embodiment, the binding sites of the microarray are DNA or DNA "mimics" (e.g., derivatives and analogues) corresponding to at least a portion of each gene in an organism's genome. In another embodiment, the binding sites of the microarray are complementary RNA or RNA mimics.

DNA mimics are polymers composed of subunits capable of specific, Watson-Crick-like hybridization with DNA, or of specific hybridization with RNA. The nucleic acids can be modified at the base moiety, at the sugar moiety, or at the phosphate backbone. Exemplary DNA mimics include, e.g., phosphorothioates.

DNA can be obtained, e.g., by polymerase chain reaction ("PCR") amplification of gene segments from genomic DNA, cDNA (e.g., by RT-PCR), or clones sequences. PCR primers are preferably chosen based on known sequences of the genes or cDNA that result in amplification of unique fragments (e.g., fragments that do not share more than 10 bases of contiguous identical sequence with any other fragment on the microarray). Computer programs that are well known in the art are useful in the design of primer with the required specificity and optimal amplification properties, such as *Oligo* version 5.0 (National Biosciences). Typically, each binding site of the microarray will be between about 20 bases and about 12,000 bases, and usually between about 300 bases and about 2,000 bases in length, and still more usually between about 300 bases and about 800 bases in length. PCR methods are well known in the art, and are described, for example, in Innis *et al.*, eds., 1990, *PCR Protocols: A Guide to Methods and Applications*, Academic Press Inc., San Diego, CA. It will be apparent to one skilled in the art that controlled robotic systems are useful for isolating and amplifying nucleic acids. In a specific embodiment of the invention, PCR methods are used to amplify ORFs of *S. cerevisiae* yeast genome. In a further preferred specific embodiment, amplification of yeast genome is performed such that each of the known or predicted ORFs in the yeast genome is prepared.

An alternative means for generating the polynucleotide binding sites of the microarray is by synthesis of synthetic polynucleotides or oligonucleotides, e.g., using N-

phosphonate or phosphoramidite chemistries (Froehler *et al.*, 1986, *Nucleic Acid Res.* 14:5399-5407; McBrid *et al.*, 1983, *Tetrahedron Lett.* 24:246-248). Synthetic sequences are typically between about 15 and about 500 bases in length, more typically between about 20 and about 50 bases. In some embodiments, synthetic nucleic acids include non-natural
5 bases, such as, but by no means limited to, inosine. As noted above, nucleic acid analogues may be used as binding sites for hybridization. An example of a suitable nucleic acid analogue is peptide nucleic acid (see, *e.g.*, Egholm *et al.*, 1993, *Nature* 363:566-568; U.S. Patent No. 5,539,083).

In alternative embodiments, the hybridization sites (*i.e.*, the binding sites) are
10 made from plasmid or phage clones of genes, cDNAs (*e.g.*, expressed sequence tags), or inserts therefrom (Nguyen *et al.*, 1995, *Genomics* 29:207-209).

5.4.2. ATTACHING BINDING SITES TO THE SOLID SURFACE

Solid supports on which binding sites of microarrays may be immobilized
15 are well-known in the art and include filter materials, such as nitrocellulose, cellulose acetate, nylon, and polyester, among others, as well as non-porous materials, such as glass, plastic (*e.g.*, polypropylene), polyacrylamide, and silicon. In general, non-porous supports, and glass in particular, are preferred. The solid support may also be treated in such a way as to enhance binding of oligonucleotides thereto, or to reduce non-specific binding of
20 unwanted substances thereto. For example, it is often desirable to treat a glass support with polylysine or silane to facilitate attachment of binding sites such as oligonucleotides to the glass. A preferred method for attaching binding sites such as nucleic acids to a surface is by printing on glass plates, as is described generally by Schena *et al.*, 1995, *Science* 270:467-470. This method is especially useful for preparing microarrays of cDNA (*See also*, DeRisi
25 *et al.*, 1996, *Nature Genetics* 14:457-460; Shalon *et al.*, 1996, *Genome Res.* 6:689-645; and Schena *et al.*, 1995, *Proc. Natl. Acad. Sci. U.S.A.* 93:10539-11286). Blanchard discloses the use of an ink jet printer for oligonucleotide synthesis (U.S. Application Serial No. 09/008,120, filed Jan. 16, 1998).

Methods of immobilizing binding sites on the solid support may include
30 direct touch, micropipetting (Yershov, K *et al.*, *Genetics* 93: 4913, 1996), or the use of controlled electric fields to direct a given oligonucleotide to a specific spot in the array (U.S. Patent 5,605,662 issued to Heller *et al.*). In a specific embodiment, DNA is typically immobilized at a density of 100 to 10,000 oligonucleotides per cm² and preferably at a density of about 1000 oligonucleotides per cm²

35 In a preferred embodiment, binding sites (*e.g.*, oligonucleotides) are synthesized directly on said support (Maskos, U *et al.*, 1993, *Nucl. Acids Res.* 21: 2267;

Fodor, S. P et al., 1991, *Science* 281:767; Blanchard et al., 1996, *Biosens. Bioelectron.* 11: 687). Among methods of synthesizing oligonucleotides directly on a solid support, particularly preferred method are photolithography (see e.g., Fodor, *supra.*, and McGall et al., 1996, *Proc. Natl. Acad. Sci. (USA)* 93: 13555, 1996) and most preferred, piezoelectric printing (see e.g., Blanchard, *supra.*).

A second preferred method for making microarrays is by making high-density oligonucleotide arrays. Techniques are known for producing arrays containing thousands of oligonucleotides complementary to defined sequences, at defined locations on a surface using photolithographic techniques for synthesis *in situ* (see, Fodor et al., 1991, *Science* 251:767-773; Pease et al., 1994, *Proc. Natl. Acad. Sci. U.S.A.* 91:5022-5026; Lockhart et al., 1996, *Nature Biotechnology* 14:1675; U.S. Patent Nos. 5,578,832; 5,556,752; and 5,510,270) or other methods for rapid synthesis and deposition of defined oligonucleotides (Blanchard et al., *Biosensors & Bioelectronics* 11:687-690). When these methods are used, oligonucleotides (e.g., 20-mers) of known sequence are synthesized directly on a surface such as a derivatized glass slides. Usually, the array produced is redundant, with several oligonucleotide molecules per RNA. Oligonucleotide binding sites can be chosen to detect alternatively spliced mRNAs.

Other methods for making microarrays, e.g., by masking (Maskos and Southern, 1992, *Nuc. Acids. Res.* 20:1679-1684), may also be used. In principle, any type of array, for example, dot blots on a nylon hybridization membrane (see Sambrook et al., *supra*) could be used. However, as will be recognized by those skilled in the art, very small arrays will frequently be preferred because hybridization volumes will be smaller.

5.4.3. TARGET POLYNUCLEOTIDES MOLECULES

As described, *supra*, the polynucleotide molecules which may be analyzed by the present invention may be from any source, including naturally occurring nucleic acid molecules, as well as synthetic nucleic acid molecules. In a preferred embodiment, the polynucleotide molecules analyzed by the invention comprise RNA, including, but by no means limited to, total cellular RNA, poly(A)⁺ messenger RNA (mRNA), fractions thereof, or RNA transcribed from cDNA. In a specific embodiment, Cellular RNA or DNAs from two cell populations (e.g., RNA of *S. cerevisiae* untreated or treated with a specific drug) are analyzed by incubating both populations of RNAs with the microarray. In a specific embodiment of the invention, *S. cerevisiae* concentrated or treated with a drug or agent known to alter the ergosterol pathway (e.g., clotrimazole). In yet another specific embodiment, *S. cerevisiae* containing a deletion mutation is used to identify gene function. Methods for preparing total and poly(A)⁺ RNA are well known in the art, and are described

generally, *e.g.*, in Sambrook *et al.*, *supra*. In one embodiment, RNA is extracted from cells of the various types of interest in this invention using guanidinium thiocyanate lysis followed by CsCl centrifugation (Chirgwin *et al.*, 1979, *Biochemistry* 18:5294-5299). Poly (A)⁺ RNA is selected by selection with oligo-dT cellulose. Cells of interest include, but are
5 by no means limited to, wild-type cells, drug-exposed wild-type cells, modified cells, diseased cells, and, in particular, cancer cells.

In one embodiment, RNA can be fragmented by methods known in the art, *e.g.*, by incubation with ZnCl₂, to generate fragments of RNA. In one embodiment, isolated mRNA can be converted to antisense RNA synthesized by *in vitro* transcription of double-
10 stranded cDNA in the presence of labeled dNTPs (Lockhart *et al.*, 1996, *Nature Biotechnology* 14:1675).

In other embodiments, the polynucleotide molecules to be analyzed may be DNA molecules such as fragmented genomic DNA, or PCR products of amplified mRNA or cDNA. In a preferred embodiment of the invention the polynucleotide molecules to be
15 analyzed are cDNAs which are reverse transcribed from mRNAs. In a specific embodiment of the invention the polynucleotide molecules analyzed are cDNAs reverse transcribed from cDNAs of fungal cell treated with antifungal drugs.

5.4.4. HYBRIDIZATION POLYNUCLEOTIDES TO MICROARRAYS

20 Nucleic acid hybridization and wash conditions are chosen so that the polynucleotide molecules to be analyzed by the invention "specifically bind" or "specifically hybridize" to the complementary polynucleotide sequences of the array, preferably to a specific array site, wherein its complementary DNA is located.

25 Arrays containing double-stranded binding site DNA situated thereon are preferably subjected to denaturing conditions to render the DNA single-stranded prior to contacting with the target polynucleotide molecules. Arrays containing single-stranded binding site DNA (*e.g.*, synthetic oligodeoxyribonucleic acids) may need to be denatured prior to contacting with the target polynucleotide molecules, *e.g.*, to remove hairpins or
30 dimers which form due to self complementary sequences.

Optimal hybridization conditions will depend on the length (*e.g.*, oligomer versus polynucleotide greater than 200 bases) and type (*e.g.*, RNA or DNA) of binding site and target nucleic acids. General parameters for specific (*i.e.*, stringent) hybridization conditions are described in Sambrook *et al.* (*supra*), and in Ausubel *et al.*, 1987, *Current
35 Protocols in Molecular Biology*, Greene Publishing and Wiley-Interscience, New York. When the cDNA microarrays of Schena *et al.* (Shena *et al.*, 1996, *Proc. Natl. Acad. Sci. U.S.A.* 93:10614) are used, typical hybridization conditions are hybridization in 5x SSC

plus 0.2% SDS at 65 °C for four hours, followed by washes at 25 °C in high stringency wash buffer (0.1x SSC plus 0.2% SDS) (Shena *et al.*, 1996, *Proc. Natl. Acad. Sci. U.S.A.* 93:10614). Useful hybridization conditions are also provided, *e.g.*, Tijessen, 1993, *Hybridization With Nucleic Acid Probes*, Elsevier Science Publishers B.V.; and Kricka, 1992, *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, CA.

In a another specific embodiment, use of a nucleic acid which is hybridizable to an *S. cerevisiae* nucleic acid or to its reverse complement, or to a nucleic acid encoding an ergosterol derivative, or to its reverse complement, under conditions of low stringency is provided. By way of example and not limitation, procedures using such conditions of low stringency are as follows (*see also* Shilo and Weinberg, 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78, 6789-6792). Arrays containing DNA are pretreated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 µg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 10⁶ cpm ³²P-labeled probe is used. Arrays are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Arrays are blotted dry and visualized. If necessary, arrays are washed for a third time at 65-68°C and re-visualized. Other conditions of low stringency which may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations).

In another specific embodiment, use of a nucleic acid which is hybridizable to an ergosterol nucleic acid, or its reverse complement, under conditions of high stringency is provided. By way of example and not limitation, procedures using such conditions of high stringency are as follows. Prehybridization of arrays containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Arrays are hybridized for 48 h at 65°C in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of arrays is done at 37°C for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50°C for 45 min before autoradiography. Other conditions of high stringency which may be used are well known in the art.

In another specific embodiment, use of a nucleic acid which is hybridizable to an ergosterol nucleic acid, or its reverse complement, under conditions of moderate

stringency is provided. Selection of appropriate conditions for such stringencies is well known in the art (*see e.g.*, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; *see also*, Ausubel et al., eds., in the Current Protocols in Molecular Biology series of laboratory
5 technique manuals, © 1987-1997, Current Protocols, © 1994-1997 John Wiley and Sons, Inc.).

In another embodiment, after hybridization, stringency conditions are as follows. Each array is washed two times each for 30 minutes each at 45°C in 40 mM sodium phosphate, pH 7.2, 5% SDS, 1 mM EDTA, 0.5% bovine serum albumin, followed
10 by four washes each for 30 minutes in sodium phosphate, pH 7.2, 1% SDS, 1 mM EDTA, and subsequently each array is treated differently as described below for low, medium, or high stringency hybridization conditions. For low stringency hybridization, arrays are not washed further. For medium stringency hybridization, membranes are additionally subjected to four washes each for 30 minutes in 40 mM sodium phosphate, pH 7.2, 1%
15 SDS, 1 mM EDTA at 55°C. For high stringency hybridization, following the washes for low stringency, membranes are additionally subjected to four washes each for 30 minutes in 40 mM sodium phosphate, pH 7.2, 1% SDS, 1 mM EDTA at 55°C, followed by four washes each for 30 minutes in sodium phosphate, pH 7.2, 1% SDS, 1 mM EDTA at 65°C.

Use of nucleic acids encoding derivatives and analogs of ergosterol-pathway
20 proteins, and ergosterol antisense nucleic acids for antifungal therapies or drug targets are additionally provided.

Use of fragments of ergosterol nucleic acids comprising regions conserved between (*i.e.*, with homology to) other ergosterol nucleic acids, of the same or different species, are also provided.

25

5.4.5. SIGNAL DETECTION ON HYBRIDIZED MICROARRAYS AND DATA ANALYSIS

It will be appreciated that when cDNA complementary to the mRNA of a cell is made and hybridized to a microarray under suitable hybridization conditions, the
30 level of hybridization to the site in the array corresponding to any particular gene will reflect the prevalence in the cell of mRNA transcribed from that gene. For example, when detectably labeled (*e.g.*, with a fluorophore) cDNA complementary to the total cellular mRNA is hybridized to a microarray, the site on the array corresponding to a gene (*i.e.*, capable of specifically binding the product of the gene) that is not transcribed in the cell will
35 have little or no signal (*e.g.*, fluorescent signal), and a gene for which the encoded mRNA is prevalent will have a relatively strong signal.

In preferred embodiments, cDNAs from two different cells (e.g. untreated and drug treated) are hybridized to the binding sites of the microarray. In the case of drug responses, one cell is exposed to a drug and another cell of the same type is not exposed to the drug. The cDNA derived from each of the two cell types are differently labeled so that they can be distinguished. In one embodiment, for example, cDNA from a cell treated with a drug is synthesized using a fluorescein-labeled dNTP, and cDNA from a second cell, not drug-exposed, is synthesized using a rhodamine-labeled dNTP. When the two cDNAs are mixed and hybridized to the microarray, the relative intensity of signal from each cDNA set is determined for each site on the array, and any relative difference in abundance of a particular mRNA is thereby detected.

In the example described above, the cDNA from the drug-treated cell will fluoresce green when the fluorophore is stimulated, and the cDNA from the untreated cell will fluoresce red. As a result, when the drug treatment has no effect, either directly or indirectly, on the relative abundance of a particular mRNA in a cell, the mRNA will be equally prevalent in both cells, and, upon reverse transcription, red-labeled and green-labeled cDNA will be equally prevalent. When hybridized to the microarray, the binding site(s) for that species of RNA will emit wavelength characteristic of both fluorophores. In contrast, when the drug-exposed cell is treated with a drug that, directly or indirectly, increases the prevalence of the mRNA in the cell, the ratio of green to red fluorescence will increase. When the drug decreases the mRNA prevalence, the ratio will decrease.

The use of a two-color fluorescence labeling and detection scheme to define alterations in gene expression has been described, (See, e.g., Shena et al., 1995, Science 270:467-470). An advantage of using cDNA labeled with two different fluorophores is that a direct and internally controlled comparison of the mRNA levels corresponding to each arrayed gene in two cell states can be made, and variations due to minor differences in experimental conditions (e.g., hybridization conditions) will not affect subsequent analyses. However, it will be recognized that it is also possible to use cDNA from a single cell, and compare, for example, the absolute amount of a particular mRNA in, e.g., a drug-treated or pathway-perturbed cell and an untreated cell.

When fluorescently labeled probes are used, the fluorescence emissions at each site of a transcript array can be, preferably, detected by scanning confocal laser microscopy (see e.g., Fodor, S., et al., 1993, Nature 364:555). In one embodiment, a separate scan, using the appropriate excitation line, is carried out for each of the two fluorophores used. Among fluorescent dyes that may be used to label DNA and RNA are fluorescein, lissamine, Cy3, Cy5, phycoerythrin, and rhodamine 110. Cy3 and Cy5 are particularly preferred. In a specific embodiment, where the sample to be hybridized is a

cDNA, labeling is accomplished by incorporating fluorescently-labeled deoxynucleotide triphosphates (dNTPs), such as Cy3 or Cy5-dUTP, during *in vitro* reverse transcription. Fluorescently-labeled dNTPs are commercially available from sources such as Amersham Pharmacia Biotech, Piscataway, NJ. Alternatively, cDNAs are labeled indirectly by
5 incorporating biotinylated nucleotides during cDNA synthesis, followed by the addition of fluorescently-labeled avidin or streptavidin. Biotinylated dNTPs are available from Enzo (Farmingdale, NY) and Boehringer Mannheim (Indianapolis, IN), while fluorescently-labeled avidin and streptavidin are available from Becton Dickinson (Mountain View, CA) and Molecular Probes (Eugene, OR). Methods of reverse transcription and labeling are
10 well-known in the art and are described for example, in Ausbel, F. et al., eds., 1994, *Current Protocols in Molecular Biology*, New York; DeRisi, J., 1997, *Science* 278:680-86; and Schena, M., et al., 1996, *Proc. Natl. Acad. Sci., USA*, 93:10614-19.

Alternatively, a laser can be used that allows simultaneous specimen illumination at wavelengths specific to the two fluorophores and emissions from the two
15 fluorophores can be analyzed simultaneously (see Shalon *et al.*, 1996, *Genome Res.* 6:639-645). In a preferred embodiment, the arrays are scanned with a laser fluorescent scanner with a computer controlled X-Y stage and a microscope objective. Although simultaneous hybridization of differentially labeled cDNA samples is preferred, use of a single label to perform hybridizations sequentially rather than simultaneously, may also be performed.
20 Sequential excitation of the two fluorophores is achieved with a multi-line, mixed gas laser, and the emitted light is split by wavelength and detected with two photomultiplier tubes. Such fluorescence laser scanning devices are described, *e.g.*, in Schena *et al.*, 1996, *Genome Res.* 6:639-645. Alternatively, the fiber-optic bundle described by Ferguson *et al.*, 1996, *Nature Biotech.* 14:1681-1684, may be used to monitor mRNA abundance levels at a large
25 number of sites simultaneously.

In one embodiment, where the sample to be hybridized is mRNA, labeling is accomplished by incorporating fluorescently-labeled ribonucleotides or biotinylated ribonucleotides during *in vitro* transcription, as described in Lockhart, D.J. et al., 1996, *Nature Biotech.* 14:1675-80.

30 Although it is preferred to use fluorescent labels, other labels may also be employed, such as radioisotopes, enzymes, and luminescers. Such methods are well-known to those of skill in the art.

To probe a DNA microarray, the labeled samples are hybridized to the microarray under a fixed set of conditions, such as sample concentration, temperature,
35 buffer and salt concentration, incubation time, etc (*see e.g.*, Section 5.4.4, herein). After washing to remove unbound sample, the microarray is excited with specific wavelengths of

light and scanned to detect fluorescence. Typically, two samples, each labeled with a different fluor, are hybridized simultaneously to permit differential expression measurements. When neither sample hybridizes to a given spot in the array, no fluorescence is detected. When only one sample hybridizes to a given spot, the color of the resulting
5 fluorescence will correspond to that of the fluor used to label the hybridizing sample (e.g., green when the sample was labeled with fluorescein, or red, if the sample was labeled with rhodamine). When both samples hybridize to the same spot, an combinatorial color is produced (e.g., yellow if the samples were labeled with fluorescein and rhodamine). Then, applying methods of pattern recognition and data analysis as described herein and in U.S.
10 patent application serial no. 09/179,569, filed October 27, 1998, now pending, in U.S. patent application serial no. 09/220,275, filed December 23, 1998, now pending, and in U.S. patent application serial no. 09/220,142 filed December 23, 1998, now pending each of which are incorporated herein by reference in their entirety, it is possible to quantify differences in gene expression between the samples.

15 Signals are recorded and, in a preferred embodiment, analyzed by computer, e.g., using a 12 bit analog to digital board. In one embodiment, the scanned image is despeckled using a graphics program (e.g., Hijaak Graphics Suite) and then analyzed using an image gridding program that creates a spreadsheet of the average hybridization at each wavelength at each site. If necessary, an experimentally determined correction for "cross
20 talk" (or overlap) between the channels for the two fluorophores may be made. For any particular hybridization site on the transcript array, a ratio of the emission of the two fluorophores can be calculated. The ratio is independent of the absolute expression level of the cognate gene, but is useful for genes whose expression is significantly modulated by drug administration, gene deletion, or any other tested event.

25 According to the method of the invention, the relative abundance of an mRNA in two cells or cell lines is scored as a perturbation and its magnitude determined (i.e., the abundance is different in the two sources of mRNA tested) or as not perturbed (i.e., the relative abundance is the same, see U.S. Patent serial No. 09/179,569, filed October 27, 1998, U.S. Patent serial No. 09/220,142, filed December 23, 1998 now pending, U.S. Patent
30 serial No. 09/220,275 filed December 23, 1998, which are incorporated herein by reference in their entirety). As used herein, a difference between the two sources of RNA of at least a factor of about 25% (i.e., RNA is 25% more abundant in one source than in the other source), more usually about 50%, even more often by a factor of about 2 (i.e., twice as abundant), 3 (three times as abundant), or 5 (five times as abundant) is scored as a
35 perturbation. Present detection methods allow reliable detection of difference of an order of about 3-fold to about 5-fold, but more sensitive methods are expected to be developed.

Preferably, in addition to identifying a perturbation as positive or negative, it is advantageous to determine the magnitude of the perturbation. This can be carried out, as noted above, by calculating the ratio of the emission of the two fluorophores used for differential labeling, or by analogous methods that will be readily apparent to those of skill
5 in the art.

5.4.6. OTHER METHODS OF TRANSCRIPTIONAL STATE MEASUREMENT

The transcriptional state of a cell may be measured by other gene expression
10 technologies known in the art. Several such technologies produce pools of restriction fragments of limited complexity for electrophoretic analysis, such as methods combining double restriction enzyme digestion with phasing primers (see, *e.g.*, European Patent O 534858 A1, filed September 24, 1992, by Zabeau *et al.*), or methods selecting restriction fragments with sites closest to a defined mRNA end (*see e.g.*, Prashar *et al.*, 1996, Proc.
15 Natl. Acad. Sci. U.S.A. 93:659-663). Other methods statistically sample cDNA pools, such as by sequencing sufficient bases (*e.g.*, 20-50 bases) in each of multiple cDNAs to identify each cDNA, or by sequencing short tags (*e.g.*, 9-10 bases) which are generated at known positions relative to a defined mRNA end (*see e.g.*, Velculescu, 1995, Science 270:484-487).

20 Such methods and systems of measuring transcriptional state, although less preferable than microarrays, may, nevertheless, be used in the present invention.

5.4.7. MEASUREMENT OF OTHER ASPECTS OF BIOLOGICAL STATE

In various embodiments of the present invention, aspects of the biological
25 state other than the transcriptional state, such as the translational state, the activity state, or mixed aspects can be measured in order to obtain drug and pathway responses. Details of these embodiments are described in this section.

5.4.7.1. EMBODIMENTS BASED ON TRANSLATIONAL STATE MEASUREMENTS

30

Measurement of the translational state may be performed according to several methods. For example, whole genome monitoring of protein (*i.e.*, the "proteome," Goffeau *et al.*, supra) can be carried out by constructing a microarray in which binding sites comprise immobilized, preferably monoclonal, antibodies specific to a plurality of protein
35 species encoded by the cell genome. Preferably, antibodies are present for a substantial fraction of the encoded proteins, or at least for those proteins relevant to the action of a drug

of interest. Methods for making monoclonal antibodies are well known (see, e.g., Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor, New York, which is incorporated in its entirety for all purposes). In a preferred embodiment, monoclonal antibodies are raised against synthetic peptide fragments designed based on genomic
5 sequence of the cell. With such an antibody array, proteins from the cell are contacted to the array and their binding is assayed with assays known in the art.

Alternatively, proteins can be separated by two-dimensional gel electrophoresis systems. Two-dimensional gel electrophoresis is well-known in the art and typically involves iso-electric focusing along a first dimension followed by SDS-PAGE
10 electrophoresis along a second dimension. See, e.g., Hames *et al.*, 1990, *Gel Electrophoresis of Proteins: A Practical Approach*, IRL Press, New York; Shevchenko *et al.*, 1996, *Proc. Nat'l Acad. Sci. USA* 93:1440-1445; Sagliocco *et al.*, 1996, *Yeast* 12:1519-1533; Lander, 1996, *Science* 274:536-539. The resulting electropherograms can be analyzed by numerous techniques, including mass spectrometric techniques, western
15 blotting and immunoblot analysis using polyclonal and monoclonal antibodies, and internal and N-terminal micro-sequencing. Using these techniques, it is possible to identify a substantial fraction of all the proteins produced under given physiological conditions, including in cells (e.g., in yeast) exposed to a drug, or in cells modified by, e.g., deletion or over-expression of a specific gene.

20

5.4.7.2. EMBODIMENTS BASED ON OTHER ASPECTS OF THE BIOLOGICAL STATE

Even though methods of this invention are illustrated by embodiments involving gene expression profiles, the methods of the invention are applicable to any
25 cellular constituent that can be monitored.

In particular, where activities of proteins relevant to the characterization of a perturbation, such as drug action, can be measured, embodiments of this invention can be based on such measurements. Activity measurements can be performed by any functional, biochemical, or physical means appropriate to the particular activity being characterized.
30 Where the activity involves a chemical transformation, the cellular protein can be contacted with the natural substrate(s), and the rate of transformation measured. Where the activity involves association in multimeric units, for example association of an activated DNA binding complex with DNA, the amount of associated protein or secondary consequences of the association, such as amounts of mRNA transcribed, can be measured. Also, where only
35 a functional activity is known, for example, as in cell cycle control, performance of the function can be observed. However known and measured, the changes in protein activities form the response data analyzed by the foregoing methods of this invention.

In alternative and non-limiting embodiments, response data may be formed of mixed aspects of the biological state of a cell. Response data can be constructed from, *e.g.*, changes in certain mRNA abundances, changes in certain protein abundances, and changes in certain protein activities.

5

5.5. DRUG DEVELOPMENT WITH TARGET GENES

The invention provides methods for the identification of target genes which may be used for the development of drugs and therapeutic agents that target a pathway of interest. By way of example, the invention is illustrated in terms of an ergosterol-pathway target gene; however, one skilled in the art will appreciate that the methods described herein may be applied to any pathway of interest and used for the development of drugs and/or therapeutic agents which target the pathway of interest. For example, one pathway of interest is the ergosterol-pathway of yeast. As described above, a target gene, for a pathway such as the ergosterol-pathway may be identified by the methods of the invention, (*e.g.*, by using cluster analysis followed by validation of the gene as a target). Target genes of the ergosterol-pathway, may be used in controlling fungal infection of human, animal, or plant species. For example, the proteins encoded by a novel target gene of the ergosterol-pathway provide targets for antifungal and fungicidal agents. For example, a drug may be developed to inhibit an essential ergosterol-pathway target gene or the protein encoded by such a gene. Inhibition of an essential target gene or protein thus modifies the growth, reproduction, and/or survival of a fungus containing the essential target gene, and thus is used as antifungal or fungicidal agent. In yet another embodiment, the drug of therapeutic agent is a dominant negative form of an ergosterol-pathway protein, which inactivates the protein encoded by the target gene of the ergosterol-pathway and may be used as an antifungal or fungicidal agent. In yet another embodiment, antisense ergosterol-pathway nucleic acids may be used to inactivate an essential target gene, and therefore provide an antifungal or fungicidal agent. Further, as will be appreciated by one skilled in the art, when a target gene is discovered by the methods of the invention, such a target may be found in species other than that which the target gene was first discovered, and may provide useful drug targets in such species. For example, if a target gene of the ergosterol-pathway is discovered in *S. cerevisiae* this gene is not only a target for antifungal or fungicidal drug development against the *S. cerevisiae*, but may lead to the development of antifungal or fungicidal agents for other fungal species as well.

Fungi which may used or tested in connection with the methods of the invention include but are not limited to: *Cryptococcus* species, including *Cryptococcus neoformans*; *Blastomyces* species, including *Blastomyces dermatitidis*; *Aiellomyces* species,

including *Aiellomyces dermatitidis*; *Histoplasma* species, including *Histoplasma capsulatum*; *Coccidioides* species, including *Coccidioides immitis*; *Candida* species, including *C. albicans*, *C. tropicalis*, *C. parapsilosis*, *C. guilliermondii*, and *C. krusei*, *Aspergillus* species, including *A. fumigatus*, *A. flavus*, and *A. niger*, *Rhizopus* species;
 5 *Rhizomucor* species; *Cunninghamella* species; *Apophysomyces* species, including *A. saksenaea*, *A. mucor*, *A. absidia*; *Sporothrix* species, including *Sporothrix schenckii*; *Paracoccidioides* species, including *Paracoccidioides brasiliensis*; *Pseudallescheria* species, including *Pseudallescheria boydii*; *Torulopsis* species, including *Torulopsis glabrata*; *Dermatophyres* species; *Histoplasma* species; *Pneumocystis* species; *Blastomyces*
 10 species; *Penicillium* species; *Microsporum* species; *Epidermophyton* species; *Trichophyton* species; *Saccharomyces* species, including *S. cerevisiae*; *Schizomyces* species, including *S. pombe*; *Trichosporon* species; *Rhodotorula* species; and *Malassezia* species.

Tests for antifungal activities can be any method known in the art. Such methods may include contacting one or more test fungal cells with the potential antifungal
 15 drug and measuring the growth inhibition or death of the fungal cells. A drug which exhibits a high rate of killing of the test fungus at low dose is a preferred antifungal drug. In one embodiment, the antifungal drug kills 50-75% of the test fungal cells. In another embodiment, the antifungal drug kills 75-85% of the test fungal cells. In a preferred embodiment, the antifungal drug kills 85-95% of the test fungal cells. In a more preferred
 20 embodiment, the antifungal drug kills 95-99% of the test fungal cells. In a most preferred embodiment, the antifungal drug kills 100% of the test fungal cells. In other embodiments of the invention, the dose of the drug is in the range of 1-10 nM, 10-100 nM, 100-1000nM, 1-10μM, 10-100μM, or 10-100μM.

As will be appreciated by one skilled in the art, any target gene may be tested
 25 for its requirement for normal activity of a pathway in order to develop a drug or therapeutic directed to the pathway in which that target gene is involved. Further, it will be appreciated that targets which are found in one species may also be a target in other species, and may be validated by the methods of the invention.

30 5.6. EXPRESSION OF REPORTER GENES AND/OR TARGET GENES

The nucleotide sequence coding for reporter gene or target gene of the invention or a functionally active analog or fragment or other derivative thereof may be used for example for the preparation of an assay in which to screen potential drugs which bind to, or enhance, inhibit, or modulate the activity of such a protein, and are described herein
 35 below. In one embodiment, the sequence can be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and

translation of the inserted protein-coding sequence. The necessary transcriptional and translational signals can also be supplied by the native ergosterol-pathway gene and/or its flanking regions. A variety of host-vector systems may be utilized to express the protein-coding sequence. These include but are not limited to mammalian cell systems infected with virus (*e.g.*, vaccinia virus, adenovirus, *etc.*); insect cell systems infected with virus (*e.g.*, baculovirus); microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

10 In yet another embodiment, a fragment of an reporter or target protein comprising one or more domains of the reporter or target protein is expressed.

In a specific embodiment, a vector is used that comprises a promoter operably linked to a nucleic acid of a reporter gene or target gene, one or more origins of replication, and, optionally, one or more selectable markers (*e.g.*, an antibiotic resistance gene).

15 In other specific embodiments, the reporter or target protein, fragment, analog, or derivative may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analog, or derivative joined via a peptide bond to a heterologous protein sequence (of a different protein)). A chimeric protein may include fusion of the reporter or target protein, fragment, analog, or derivative to a second protein or at least a

20 portion thereof, wherein a portion is one (preferably 10, 15, or 20) or more amino acids of said second protein. Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made

25 by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer.

The invention provides a method for identifying a molecule that modulates the expression of an ergosterol-pathway gene selected from the group consisting of YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5),

30 YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9), comprising recombinantly expressing in a fungal cell one or more candidate molecules, and detecting the expression of said ergosterol-pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates

35 ergosterol-pathway gene expression.

The invention provides a method for identifying a molecule that modulates the expression of a PKC-pathway gene selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21), comprising recombiningly expressing in a fungal cell one or more candidate molecules, and detecting the expression of said PKC-pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates PKC-pathway gene expression.

The invention provides a method for identifying a molecule that modulates the expression of an Invasive Growth pathway gene selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29), comprising recombiningly expressing in a fungal cell one or more candidate molecules, and detecting the expression of said Invasive Growth pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates Invasive Growth pathway gene expression.

5.7. STRUCTURE OF REPORTER AND/OR TARGET GENES AND PROTEINS

The structure of reporter or target genes and proteins of the invention can be analyzed by various methods known in the art. Such analysis may be useful, for example, in the design of antifungal or fungicidal agents of the invention. Some examples of such methods are described below.

5.7.1. GENETIC ANALYSIS

The cloned DNA or cDNA corresponding to a reporter or target gene can be analyzed by methods including but not limited to Southern hybridization (Southern, 1975, J. Mol. Biol. 98:503-517), Northern hybridization (*see e.g.*, Freeman et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:4094-4098), restriction endonuclease mapping (Maniatis, 1982, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), and DNA sequence analysis. Accordingly, this invention provides for the use of nucleic acid probes recognizing a reporter or target gene. For

example, polymerase chain reaction (PCR; U.S. Patent Nos. 4,683,202, 4,683,195 and 4,889,818; Gyllenstein et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7652-7656; Ochman et al., 1988, Genetics 120:621-623; Loh et al., 1989, Science 243:217-220) followed by Southern hybridization with an a reporter or target gene-specific probe can allow the
5 detection of a reporter or target gene in DNA from various cell types. In one specific embodiment, the cell types are from different species within the same phylogenetic kingdom. Methods of amplification other than PCR are commonly known and can also be employed. In one embodiment, Southern hybridization can be used to determine the genetic linkage of a reporter or target gene. Northern hybridization analysis can be used to
10 determine the expression of a gene assigned to the a particular biological pathway by the methods disclosed herein. Various cell types, at various states of development or activity can be tested for gene expression. The stringency of the hybridization conditions for both Southern and Northern hybridization can be manipulated to ensure detection of nucleic acids with the desired degree of relatedness to the specific a reporter or target gene probe used.
15 Modifications of these methods and other methods commonly known in the art can be used.

Restriction endonuclease mapping can be used to roughly determine the genetic structure of a reporter or target gene. Restriction maps derived by restriction endonuclease cleavage can be confirmed by DNA sequence analysis. Restriction endonucleases may also be used to digest DNA sequences which are attached to
20 microarrays.

DNA sequence analysis can be performed by any techniques known in the art, including but not limited to the method of Maxam and Gilbert (1980, Meth. Enzymol. 65:499-560), the Sanger dideoxy method (Sanger et al., 1977, Proc. Natl. Acad. Sci. U.S.A. 74:5463), the use of T7 DNA polymerase (Tabor and Richardson, U.S. Patent No.
25 4,795,699), or use of an automated DNA sequencer (e.g., Applied Biosystems, Foster City, California). In a specific embodiment, DNA sequencing is used to confirm the sequence of a microarray binding partner or probe.

5.7.2. PROTEIN ANALYSIS

30 The amino acid sequence of an ergosterol-pathway protein can be derived by deduction from the DNA sequence, or alternatively, by direct sequencing of the protein, e.g., with an automated amino acid sequencer. In a preferred embodiment, *S. cerevisiae* protein sequences are obtained thru the Saccharomyces Genome Database (www.Stratford.edu/Saccharomyces).

35 A reporter-gene or target-gene protein sequence can be further characterized by a hydrophilicity analysis (Hopp and Woods, 1981, Proc. Natl. Acad. Sci. U.S.A.

78:3824). A hydrophilicity profile can be used to identify the hydrophobic and hydrophilic regions of the protein encoded by a reporter gene or target gene and the corresponding regions of the gene sequence which encode such regions.

- 5 Structural prediction analysis (Chou and Fasman, 1974, Biochemistry 13:222) can also be done, to identify regions of a protein encoded by a reporter gene or target gene, that assume specific secondary structures, which may be useful in the design of therapeutics which target specific biological-pathway proteins.

10 Manipulation, translation, and secondary structure prediction, open reading frame prediction and plotting, as well as determination of sequence homologies, can also be accomplished using computer software programs available in the art.

- 15 Other methods of structural analysis can also be employed. These include but are not limited to X-ray crystallography (Engstrom, 1974, Biochem. Exp. Biol. 11:7-13), nuclear magnetic resonance spectroscopy (Clare and Gonenborn, 1989, CRC Crit. Rev. Biochem. 24:479-564) and computer modeling (Fletterick and Zoller, 1986, Computer Graphics and Molecular Modeling, in *Current Communications in Molecular Biology*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

 The invention further relates to the use of proteins encoded by reporter genes or target genes, derivatives (including but not limited to fragments), analogs, and molecules of reporter or target proteins.

- 20 The production and use of fragments, derivatives, and analogs related to a reporter or target protein are within the scope of the present invention. In a specific embodiment, the derivative or analog is functionally active, *i.e.*, capable of exhibiting one or more functional activities associated with a full-length, wild-type reporter or target protein. As one example, such derivatives or analogs which have the desired re-clustering activity
25 can be assigned to a biological-pathway. As yet another example, such derivatives or analogs which have the desired co-clustering activity can be used for targets for the development of drugs directed to such a target, such as an antifungal or fungicidal agent directed to a target gene in the ergosterol-pathway. Derivatives or analogs that retain, or alternatively lack or inhibit, a desired biological-pathway protein property-of-interest (*e.g.*,
30 binding to a specific biological pathway protein binding partner), can be used as inducers, or inhibitors, respectively, of such property and its physiological correlates. A specific embodiment relates to a dominant negative form of an ergosterol-pathway protein fragment that can bind and inhibit ergosterol-pathway protein. Derivatives or analogs of an ergosterol-pathway protein can be tested for the desired activity by procedures known in the
35 art, including but not limited to the assays described below.

In particular, reporter or target protein derivatives can be made by altering the sequences by substitutions, additions (*e.g.*, insertions) or deletions. Due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as the reporter or target gene may be used in the practice of the present invention. These include but are not limited to nucleotide sequences comprising all or portions of a reporter or target gene which is altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change.

In a specific embodiment of the invention, use of proteins consisting of or comprising a fragment of reporter or target protein consisting of at least 10 (continuous) amino acids of the reporter or target protein is provided. In other embodiments, the fragment consists of at least 20 or at least 50 amino acids of the reporter or target protein. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids. Use of derivatives or analogs of reporter or target proteins include but are not limited to those molecules comprising regions that are substantially homologous to the reporter or target protein or fragment thereof (*e.g.*, in various embodiments, at least 60% or 70% or 80% or 90% or 95% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art) or whose encoding nucleic acid is capable of hybridizing to a coding reporter or target gene sequence, under high stringency, moderate stringency, or low stringency conditions.

Specifically, by way of example computer programs for determining homology may include but are not limited to TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA* 85(8):2444-8; Altschul et al., 1990, *J. Mol. Biol.* 215(3):403-10; Thompson, et al., 1994, *Nucleic Acids Res.* 22(22):4673-80; Higgins, et al., 1996, *Methods Enzymol* 266:383-402; Altschul, et al., 1990, *J. Mol. Biol.* 215(3):403-10).

Specifically, Basic Local Alignment Search Tool (BLAST) (www.ncbi.nlm.nih.gov) (Altschul et al., 1990, *J. of Molec. Biol.*, 215:403-410, "The BLAST Algorithm; Altschul et al., 1997, *Nuc. Acids Res.* 25:3389-3402) is a heuristic search algorithm tailored to searching for sequence similarity which ascribes significance using the statistical methods of Karlin and Altschul 1990, *Proc. Nat'l Acad. Sci. USA*, 87:2264-68; 1993, *Proc. Nat'l Acad. Sci. USA* 90:5873-77. Five specific BLAST programs perform the following tasks: 1) The BLASTP program compares an amino acid query sequence against a protein sequence database; 2) The BLASTN program compares a nucleotide query sequence against a nucleotide sequence database; 3) The BLASTX

program compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database; 4) The TBLASTN program compares a protein query sequence against a nucleotide sequence database translated in all six reading frames (both strands); 5) The TBLASTX program compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

Smith-Waterman (database: European Bioinformatics Institute wwwz.ebi.ac.uk/bic_sw/) (Smith-Waterman, 1981, J. of Molec. Biol., 147:195-197) is a mathematically rigorous algorithm for sequence alignments.

10 FASTA (*see* Pearson et al., 1988, Proc. Nat'l Acad. Sci. USA, 85:2444-2448) is a heuristic approximation to the Smith-Waterman algorithm. For a general discussion of the procedure and benefits of the BLAST, Smith-Waterman and FASTA algorithms *see* Nicholas et al., 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" (www.psc.edu) and references cited therein.

15 The reporter or target derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level. For example, a cloned reporter or target gene sequence can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated *in vitro*.

20 Additionally, an reporter or target gene nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or to form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to, chemical mutagenesis, *in vitro* site-directed mutagenesis (Hutchinson et al., 1978, J. Biol. Chem. 253:6551), use of TAB® linkers (Pharmacia), PCR with primers containing a
30 mutation, *etc.*

Manipulations of an reporter or target protein sequence may also be made at the protein level. Included within the scope of the invention are reporter or target protein fragments or other derivatives or analogs which are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by
35 known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, *etc.* Any of numerous chemical modifications may be carried out by

known techniques, including but not limited to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, *etc.*

In addition, analogs and derivatives of a reporter or target protein can be chemically synthesized. For example, a peptide corresponding to a portion of a reporter or target protein which comprises the desired domain, or which mediates the desired activity *in vitro*, can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the reporter or target sequence. Non-classical amino acids include but are not limited to the D-isomers of the common amino acids, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, C α -methyl amino acids, N α -methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

In a specific embodiment, an reporter or target protein derivative is a chimeric or fusion protein comprising a reporter or target protein or fragment thereof (preferably consisting of at least a domain or motif of the reporter or target protein, or at least 10 amino acids of the reporter or target protein) joined at its amino- or carboxy-terminus via a peptide bond to an amino acid sequence of a different protein. In specific embodiments, the amino acid sequence of the different protein is at least 6, 10, 20 or 30 continuous amino acids of the different proteins or a portion of the different protein that is functionally active. In one embodiment, such a chimeric protein is produced by recombinant expression of a nucleic acid encoding the protein (comprising an reporter or target-coding sequence joined in-frame to a coding sequence for a different protein). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art. Alternatively, such a chimeric product may be made by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer. Chimeric genes comprising portions of a reporter or target gene fused to any heterologous protein-encoding sequences may be constructed. A specific embodiment relates to a chimeric protein comprising a fragment of reporter or target protein of at least six amino acids, or a fragment that displays one or more functional activities of the reporter or target protein.

5.8. IDENTIFICATION OF COMPOUNDS WITH BINDING CAPACITY

This invention provides screening methodologies useful in the identification of proteins and other compounds which bind to, or otherwise directly interact with, the reporter or target genes and proteins. Screening methodologies are well known in the art
5 The proteins and compounds include endogenous cellular components which interact with the identified genes and proteins *in vivo* and which, therefore, may provide new targets for pharmaceutical and therapeutic interventions, as well as recombinant, synthetic, and otherwise exogenous compounds which may have binding capacity and, therefore, may be candidates for pharmaceutical agents. Thus, in one series of embodiments, cell lysates may
10 be screened for proteins or other compounds which bind to one of the normal or mutant reporter or target genes and proteins.

Alternatively, any of a variety of exogenous compounds, both naturally occurring and/or synthetic (*e.g.*, libraries of small molecules or peptides), may be screened
15 for binding capacity.

As will be apparent to one of ordinary skill in the art, there are numerous other methods of screening individual proteins or other compounds, as well as large libraries of proteins or other compounds (*e.g.*, phage display libraries) to identify molecules which bind to reporter or target proteins of the invention. All of these methods comprise the step
20 of mixing a reporter or target protein or fragment with test compounds, allowing time for any binding to occur, and assaying for any bound complexes. All such methods are enabled by the present disclosure of substantially pure reporter or target proteins, substantially pure functional domain fragments, fusion proteins, antibodies, and methods of making and using the same. In a specific embodiment, the reporter or target protein is an ergosterol-pathway
25 protein. In another specific embodiment, the reporter or target protein is a PKC-pathway protein. In another specific embodiment, the reporter or target protein is an Invasive Growth pathway protein.

The invention provides a method of identifying a molecule that binds to a ligand selected from the group consisting of (i) an *S. cerevisiae* ergosterol-pathway protein selected from the group consisting of YHR039C (as depicted in FIG.3, as set
30 forth in SEQ ID NO:2), YLW100W (as depicted in FIG.5, as set forth in SEQ ID NO:4), YPL272C (as depicted in FIG.7, as set forth in SEQ ID NO:6), YGR131W (as depicted in FIG.9, as set forth in SEQ ID NO:8), and YDR453C (as depicted in FIG.11, as set forth in SEQ ID NO:10), (ii) a fragment of the *S. cerevisiae* ergosterol-pathway protein, and (iii) a nucleic acid encoding the *S. cerevisiae*
35 ergosterol-pathway protein or fragment, the method comprising:(a) contacting the ligand with a plurality of molecules under conditions conducive to binding between

the ligand and the molecules; and (b) identifying a molecule within the plurality that binds to the ligand.

The invention provides a method of identifying a molecule that binds to a ligand selected from the group consisting of (i) an *S. cerevisiae* PKC-pathway protein selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.18, as set forth in SEQ ID NO:12), YKR161C (as depicted in FIG.20, as set forth in SEQ ID NO:14), PIR3(YKL163W) (as depicted in FIG.22, as set forth in SEQ ID NO:16), YPK2(YMR104C) (as depicted in FIG.24, as set forth in SEQ ID NO:18), YLR194C (as depicted in FIG.26, as set forth in SEQ ID NO:20), and ST1(YDR055W) (as depicted in FIG.28, as set forth in SEQ ID NO:22), (ii) a fragment of the *S. cerevisiae* PKC-pathway protein, and (iii) a nucleic acid encoding the *S. cerevisiae* PKC-pathway protein or fragment, the method comprising: (a) contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and (b) identifying a molecule within the plurality that binds to the ligand.

The invention provides a method of identifying a molecule that binds to a ligand selected from the group consisting of (i) an *S. cerevisiae* Invasive Growth pathway protein selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.30, as set forth in SEQ ID NO:24), PGU1(YJR153W) (as depicted in FIG.32, as set forth in SEQ ID NO:26), YRL042C (as depicted in FIG.34, as set forth in SEQ ID NO:28), and SVS1(YPL163C) (as depicted in FIG.36, as set forth in SEQ ID NO:30), (ii) a fragment of the *S. cerevisiae* Invasive Growth pathway protein, and (iii) a nucleic acid encoding the *S. cerevisiae* Invasive Growth pathway protein or fragment, the method comprising (a) contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and (b) identifying a molecule within the plurality that binds to the ligand.

5.8.1. PROTEINS WHICH INTERACT WITH PATHWAY-SPECIFIC PROTEINS

The present invention further provides methods of identifying or screening for proteins which interact with reporter or target proteins of a biological pathway of interest, or derivatives, fragments, or analogs thereof. In specific embodiments, the method of identifying a molecule that binds to a ligand (e.g., an ergosterol-pathway protein) comprises contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and identifying a molecule within the plurality that binds to the ligand. The ligand or protein in the method can either be a purified or non-purified form. Preferably, the method of identifying or screening is a yeast two-hybrid assay system or a variation thereof, as further described below. In this regard, the

yeast two-hybrid method has been used to analyze protein-protein interactions (*see e.g.* Zhu and Kahn, 1997, Proc. Natl. Acad. Sci. U.S.A. 94:13063-13068). Derivatives (*e.g.*, fragments) and analogs of a protein can also be assayed for binding to a binding partner by any method known in the art, for example, immunoprecipitation with an antibody that binds
5 to the protein in a complex followed by analysis by size fractionation of the immunoprecipitated proteins (*e.g.*, by denaturing or nondenaturing polyacrylamide gel electrophoresis), Western analysis, non-denaturing gel electrophoresis, *etc.*

One aspect of the present invention provides methods for assaying and screening fragments, derivatives and analogs of reporter or target proteins of the invention
10 for interacting proteins (*e.g.*, for binding to an *S. cerevisiae* ergosterol peptide). Derivatives, analogs and fragments of proteins that interact with a reporter or target protein can preferably identified by means of a yeast two hybrid assay system (Fields and Song, 1989, Nature 340:245-246; U.S. Patent No. 5,283,173). Because the interactions are screened for in yeast, the intermolecular protein interactions detected in this system occur
15 under physiological conditions that mimic the conditions in eukaryotic cells, including vertebrates or invertebrates (Chien et al., 1991, Proc. Natl. Acad. Sci. U.S.A. 88:9578-9581). By way of illustration, this feature facilitates identification of proteins capable of interaction with an *S. cerevisiae* ergosterol-pathway protein from species other than *S. cerevisiae*.

Identification of interacting proteins by the improved yeast two-hybrid
20 system is based upon the detection of expression of a "marker" gene, the transcription of which is dependent upon the reconstitution of a transcriptional regulator by the interaction of two proteins, each fused to one half of the transcriptional regulator. In some embodiments of the invention, the "marker" genes as described below, act as a read-out for the interaction of two test proteins called the bait and the prey. The "bait" (*i.e.*, a pathway-specific reporter
25 or target protein of a or derivative or analog thereof) and "prey" (proteins to be tested for ability to interact with the bait) proteins are expressed as fusion proteins to a DNA binding domain, and to a transcriptional regulatory domain, respectively, or *vice versa*. In various specific embodiments, the prey has a complexity of at least about 50, about 100, about 500, about 1,000, about 5,000, about 10,000, or about 50,000; or has a complexity in the range of
30 about 25 to about 100,000, about 100 to about 100,000, about 50,000 to about 100,000, or about 100,000 to about 500,000. For example, the prey population can be one or more nucleic acids encoding mutants of a protein (*e.g.*, as generated by site-directed mutagenesis or another method of making mutations in a nucleotide sequence). Preferably, the prey populations are proteins encoded by DNA, *e.g.*, cDNA or genomic DNA or synthetically-
35 generated DNA. For example, the populations can be expressed from chimeric genes

comprising cDNA sequences from an un-characterized sample of a population of cDNA from mRNA.

One characteristic of the yeast two-hybrid system is that proteins examined in this system are expressed as cytoplasmic proteins, and therefore do not pass through the secretory pathway. However, several methods are incorporated in the present invention to examine derivatives of reporter or target proteins of the invention that mimic processed forms of these proteins.

In a specific embodiment, recombinant biological libraries expressing random peptides can be used as the source of prey nucleic acids.

In another embodiment, the invention provides methods of screening for inhibitors or enhancers of the protein interactants identified herein. Briefly, the protein-protein interaction assay can be carried out as described herein, except that it is done in the presence of one or more candidate molecules. An increase or decrease in marker gene activity relative to that present when the one or more candidate molecules are absent indicates that the candidate molecule has an effect on the interacting pair. In a preferred method, inhibition of the interaction is selected for (*i.e.*, inhibition of the interaction is necessary for the cells to survive), for example, where the interaction activates the *URA3* gene, causing yeast to die in medium containing the chemical 5-fluoroorotic acid (Rothstein, 1983, Meth. Enzymol. 101:167-180). The identification of inhibitors of such interactions can also be accomplished, for example, but not by way of limitation, using competitive inhibitor assays, as described above.

In general, proteins of the bait and prey populations are provided as fusion (chimeric) proteins (preferably by recombinant expression of a chimeric coding sequence) comprising each protein contiguous to a pre-selected sequence. For one population, the pre-selected sequence is a DNA binding domain. The DNA binding domain can be any DNA binding domain, as long as it specifically recognizes a DNA sequence within a promoter. For example, the DNA binding domain is of a transcriptional activator or inhibitor. For the other population, the pre-selected sequence is an activator or inhibitor domain of a transcriptional activator or inhibitor, respectively. The regulatory domain alone (not as a fusion to a protein sequence) and the DNA-binding domain alone (not as a fusion to a protein sequence) preferably do not detectably interact (so as to avoid false positives in the assay). The assay system further includes a reporter gene operably linked to a promoter that contains a binding site for the DNA binding domain of the transcriptional activator (or inhibitor).

Accordingly, in the present method of the invention, binding of a bait fusion protein containing a reporter or target protein of the invention (such as an *S. cerevisiae*

ergosterol-pathway protein) to a prey fusion protein leads to reconstitution of a transcriptional activator (or inhibitor) which activates (or inhibits) expression of the marker gene. The activation (or inhibition) of transcription of the marker gene occurs intracellularly, *e.g.*, in prokaryotic or eukaryotic cells, preferably in cell culture.

- 5 The promoter that is operably linked to the marker gene nucleotide sequence can be a native or non-native promoter of the nucleotide sequence, and the DNA binding site(s) that are recognized by the DNA binding domain portion of the fusion protein can be native to the promoter (if the promoter normally contains such binding site(s)) or non-native to the promoter. Thus, for example, one or more tandem copies (*e.g.*, four or five copies) of
- 10 the appropriate DNA binding site can be introduced upstream of the TATA box in the desired promoter (*e.g.*, in the area of about position -100 to about -400). In a preferred aspect, 4 or 5 tandem copies of the 17 bp UAS (GAL4 DNA binding site) are introduced upstream of the TATA box in the desired promoter, which is upstream of the desired coding sequence for a selectable or detectable marker. In a preferred embodiment, the GAL1-10
- 15 promoter is operably fused to the desired nucleotide sequence; the GAL1-10 promoter already contains 4 binding sites for GAL4.

Alternatively, the transcriptional activation binding site of the desired gene(s) can be deleted and replaced with GAL4 binding sites (Bartel et al., 1993, BioTechniques 14:920-924; Chasman et al., 1989, Mol. Cell. Biol. 9:4746-4749). The marker gene

20 preferably contains the sequence encoding a detectable or selectable marker, the expression of which is regulated by the transcriptional activator, such that the marker is either turned on or off in the cell in response to the presence of a specific interaction. Preferably, the assay is carried out in the absence of background levels of the transcriptional activator (*e.g.*, in a cell that is mutant or otherwise lacking in the transcriptional activator).

- 25 In one embodiment, more than one marker gene is used to detect transcriptional activation, *e.g.*, one marker gene encoding a detectable marker and one or more marker genes encoding different selectable markers. The detectable marker can be any molecule that can give rise to a detectable signal, *e.g.*, a fluorescent protein or a protein that can be readily visualized or that is recognizable by a specific antibody. The selectable
- 30 marker can be any protein molecule that confers the ability to grow under conditions that do not support the growth of cells not expressing the selectable marker, *e.g.*, the selectable marker is an enzyme that provides an essential nutrient and the cell in which the interaction assay occurs is deficient in the enzyme and the selection medium lacks such nutrient. The marker gene can either be under the control of the native promoter that naturally contains a
- 35 binding site for the DNA binding protein, or under the control of a heterologous or synthetic promoter.

The activation domain and DNA binding domain used in the assay can be from a wide variety of transcriptional activator proteins, as long as these transcriptional activators have separable binding and transcriptional activation domains. For example, the GAL4 protein of *S. cerevisiae* (Ma et al., 1987, Cell 48:847-853), the GCN4 protein of *S. cerevisiae* (Hope and Struhl, 1986, Cell 46:885-894), the ARD1 protein of *S. cerevisiae* (Thukral et al., 1989, Mol. Cell. Biol. 9:2360-2369), and the human estrogen receptor (Kumar et al., 1987, Cell 51:941-951), have separable DNA binding and activation domains. The DNA binding domain and activation domain that are employed in the fusion proteins need not be from the same transcriptional activator. In a specific embodiment, a GAL4 or LEXA DNA binding domain is employed. In another specific embodiment, a GAL4 or herpes simplex virus VP16 (Triezenberg et al., 1988, Genes Dev. 2:730-742) activation domain is employed. In a specific embodiment, amino acids 1-147 of GAL4 (Ma et al., 1987, Cell 48:847-853; Ptashne et al., 1990, Nature 346:329-331) is the DNA binding domain, and amino acids 411-455 of VP16 (Triezenberg et al., 1988, Genes Dev. 2:730-742; Cress et al., 1991, Science 251:87-90) comprise the activation domain.

In a preferred embodiment, the yeast transcription factor GAL4 is reconstituted by protein-protein interaction and the host strain is mutant for GAL4. In another embodiment, the DNA-binding domain is Ace1N and/or the activation domain is Ace1, the DNA binding and activation domains of the Ace1 protein, respectively. Ace1 is a yeast protein that activates transcription from the *CUP1* operon in the presence of divalent copper. *CUP1* encodes metallothionein, which chelates copper, and the expression of CUP1 protein allows growth in the presence of copper, which is otherwise toxic to the host cells. The marker gene can also be a *CUP1-lacZ* fusion that expresses the enzyme beta-galactosidase (detectable by routine chromogenic assay) upon binding of a reconstituted Ace1N transcriptional activator (see Chaudhuri et al., 1995, FEBS Letters 357:221-226). In another specific embodiment, the DNA binding domain of the human estrogen receptor is used, with a marker gene driven by one or three estrogen receptor response elements (Le Douarin et al., 1995, Nucl. Acids. Res. 23:876-878).

The DNA binding domain and the transcriptional activator/inhibitor domain each preferably has a nuclear localization signal (see Ylikomi et al., 1992, EMBO J. 11:3681-3694; Dingwall and Laskey, 1991, TIBS 16:479-481) functional in the cell in which the fusion proteins are to be expressed.

To facilitate isolation of the encoded proteins, the fusion constructs can further contain sequences encoding affinity tags such as glutathione-S-transferase or maltose-binding protein or an epitope of an available antibody, for affinity purification (e.g., binding to glutathione, maltose, or a particular antibody specific for the epitope,

respectively) (Allen et al., 1995, TIBS 20:511-516). In another embodiment, the fusion constructs further comprise bacterial promoter sequences for recombinant production of the fusion protein in bacterial cells.

- The host cell in which the interaction assay occurs can be any cell, prokaryotic or eukaryotic, in which transcription of the marker gene can occur and be detected, including, but not limited to, mammalian (e.g., monkey, mouse, rat, human, bovine), chicken, bacterial, or insect cells, and is preferably a yeast cell. Expression constructs encoding and capable of expressing the binding domain fusion proteins, the transcriptional activation domain fusion proteins, and the marker gene product(s) are provided within the host cell, by mating of cells containing the expression constructs, or by cell fusion, transformation, electroporation, microinjection, *etc.* The host cell used should not express an endogenous transcription factor that binds to the same DNA site as that recognized by the DNA binding domain fusion population. Also, preferably, the host cell is mutant or otherwise lacking in an endogenous, functional form of the marker gene(s) used in the assay. Various vectors and host strains for expression of the two fusion protein populations in yeast are known and can be used (*see e.g.*, U.S. Patent No. 5,1468,614; Bartel et al., 1993, "Using the two-hybrid system to detect protein-protein interactions" In *Cellular Interactions in Development*, Hartley, ed., Practical Approach Series xviii, IRL Press at Oxford University Press, New York, NY, pp. 153-179; Fields and Sternglanz, 1994, Trends In Genetics 10:286-292). By way of example but not limitation, yeast strains or derivative strains made therefrom, which can be used are N105, N106, N1051, N1061, and YULH. Other exemplary strains that can be used in the assay of the invention also include, but are not limited to, the following:

Y190: MATa, *ura3-52*, *his3-200*, *lys2-801*, *ade2-101*, *trp1-901*, *leu2-3,112*, *gal4 α* , *gal80 α* , *cyh'2*, *LYS2::GAL1_{UAS}-HIS3_{TATA}HIS3*, *URA3::GAL1_{UAS}-GAL1_{TATA}-lacZ*; Harper et al., 1993, Cell 75:805-816, available from Clontech, Palo Alto, California. Y190 contains *HIS3* and *lacZ* marker genes driven by GAL4 binding sites.

CG-1945: MATa, *ura3-52*, *his3-200*, *lys2-801*, *ade2-101*, *trp1-901*, *leu2-3,112*, *gal4-542*, *gal80-538*, *cyh'2*, *LYS2::GAL1_{UAS}-HIS3_{TATA}HIS3*, *URA3::GAL1_{UAS}17mers(x3)-CYC1_{TATA}-lacZ*, available from Clontech, Palo Alto, California. CG-1945 contains *HIS3* and *lacZ* marker genes driven by GAL4 binding sites.

Y187: MAT- α , *ura3-52*, *his3-200*, *ade2-101*, *trp1-901*, *leu2-3,112*, *gal4 α* , *gal80 α* , *URA3::GAL1_{UAS}-GAL1_{TATA}-lacZ*, available from Clontech, Palo Alto, California. Y187 contains a *lacZ* marker gene driven by GAL4 binding sites.

SFY526: MATa, *ura3-52, his3-200, lys2-801, ade2-101, trp1-901, leu2-3,112, gal4-542, gal80-538, can^r, URA3::GAL1-lacZ*, available from Clontech, Palo Alto, California. SFY526 contains *HIS3* and *lacZ* marker genes driven by GAL4 binding sites.

HF7c: MATa, *ura3-52, his3-200, lys2-801, ade2-101, trp1-901, leu2-3,112, gal4-542, gal80-538, LYS2::GAL1-HIS3, URA3::GAL1_{UAS 17MERS(x3)}-CYC1-lacZ*, available from Clontech, Palo Alto, California. HF7c contains *HIS3* and *lacZ* marker genes driven by GAL4 binding sites.

YRG-2: MATa, *ura3-52, his3-200, lys2-801, ade2-101, trp1-901, leu2-3,112, gal4-542, gal80-538, LYS2::GAL1_{UAS}-GAL1_{TATA}-HIS3, URA3::GAL1_{UAS17mers(x3)}-CYC1-lacZ*, available from Stratagene, La Jolla, California. YRG-2 contains *HIS3* and *lacZ* marker genes driven by GAL4 binding sites. Many other strains commonly known and available in the art can be used.

If not already lacking in endogenous marker gene activity, cells mutant in the marker gene may be selected by known methods, or the cells can be made mutant in the marker gene by known gene-disruption methods prior to introducing the marker gene (Rothstein, 1983, *Meth. Enzymol.* 101:202-211).

In a specific embodiment, plasmids encoding the different fusion protein populations can be introduced simultaneously into a single host cell (e.g., a haploid yeast cell) containing one or more marker genes, by co-transformation, to conduct the assay for protein-protein interactions. Or, preferably, the two fusion protein populations are introduced into a single cell either by mating (e.g., for yeast cells) or cell fusions (e.g., of mammalian cells). In a mating type assay, conjugation of haploid yeast cells of opposite mating type that have been transformed with a binding domain fusion expression construct (preferably a plasmid) and an activation (or inhibitor) domain fusion expression construct (preferably a plasmid), respectively, will deliver both constructs into the same diploid cell. The mating type of a yeast strain may be manipulated by transformation with the HO gene (Herskowitz and Jensen, 1991, *Meth. Enzymol.* 194:132-146).

In a preferred embodiment, a yeast interaction mating assay is employed using two different types of host cells, strain-type a and alpha of the yeast *Saccharomyces cerevisiae*. The host cell preferably contains at least two marker genes, each with one or more binding sites for the DNA-binding domain (e.g., of a transcriptional activator). The activator domain and DNA binding domain are each parts of chimeric proteins formed from the two respective populations of proteins. One strain of host cells, for example the a strain, contains fusions of the library of nucleotide sequences with the DNA-binding domain of a transcriptional activator, such as GAL4. The hybrid proteins expressed in this set of host cells are capable of recognizing the DNA-binding site in the promoter or enhancer region in

the marker gene construct. The second set of yeast host cells, for example, the alpha strain, contains nucleotide sequences encoding fusions of a library of DNA sequences fused to the activation domain of a transcriptional activator.

In a preferred embodiment, the fusion protein constructs are introduced into
5 the host cell as a set of plasmids. These plasmids are preferably capable of autonomous replication in a host yeast cell and preferably can also be propagated in *E. coli*. The plasmid contains a promoter directing the transcription of the DNA binding or activation domain fusion genes, and a transcriptional termination signal. The plasmid also preferably contains a selectable marker gene, permitting selection of cells containing the plasmid. The plasmid
10 can be single-copy or multi-copy. Single-copy yeast plasmids that have the yeast centromere may also be used to express the activation and DNA binding domain fusions (Elledge et al., 1988, *Gene* 70:303-312).

In another embodiment, the fusion constructs are introduced directly into the yeast chromosome via homologous recombination. The homologous recombination for
15 these purposes is mediated through yeast sequences that are not essential for vegetative growth of yeast, e.g., the *MER2*, *MER1*, *ZIP1*, *REC102*, or *ME14* gene.

Bacteriophage vectors can also be used to express the DNA binding domain and/or activation domain fusion proteins. Libraries can generally be prepared faster and more easily from bacteriophage vectors than from plasmid vectors.

20 In a specific embodiment, the present invention provides a method of detecting one or more protein-protein interactions combined with a negative selection step as described in PCT International Publication No. WO97/47763, published December 18, 1997, which is incorporated by reference herein in its entirety.

In a preferred embodiment, the bait *S. cerevisiae* ergosterol sequence and the
25 prey library of chimeric genes are combined by mating the two yeast strains on solid media, such that the resulting diploids contain both kinds of chimeric genes, i.e., the DNA-binding domain fusion and the activation domain fusion.

Preferred marker genes include the *URA3*, *HIS3* and/or the *lacZ* genes (see e.g., Rose and Botstein, 1983, *Meth. Enzymol.* 101:167-180) operably linked to GAL4 DNA-
30 binding domain recognition elements. Other marker genes include but are not limited to, Green Fluorescent Protein (GFP) (Cubitt et al., 1995, *Trends Biochem. Sci.* 20:448-455), luciferase, *LEU2*, *LYS2*, *ADE2*, *TRP1*, *CAN1*, *CYH2*, *GUS*, *CUP1* or chloramphenicol acetyl transferase (CAT). Expression of the marker genes can be detected by techniques known in the art (see e.g. PCT International Publication No. WO97/47763, published December 18,
35 1997, which is incorporated by reference herein in its entirety).

In a specific embodiment, transcription of the marker gene is detected by a linked replication assay. For example, as described by Vasavada et al., 1991, *Proc. Natl. Acad. Sci. U.S.A.* 88:10686-10690, expression of SV40 large T antigen is under the control of the E1B promoter responsive to GAL4 binding sites. The replication of a plasmid
5 containing the SV40 origin of replication, indicates a protein-protein interaction. Alternatively, a polyoma virus replicon can be used (Vasavada et al., 1991, *Proc. Natl. Acad. Sci. U.S.A.* 88:10686-90).

In another embodiment, the expression of marker genes that encode proteins can be detected by immunoassay, *i.e.*, by detecting the immunospecific binding of an
10 antibody to such protein, which antibody can be labeled, or incubated with a labeled binding partner to the antibody, to yield a detectable signal. Alam and Cook disclose non-limiting examples of detectable marker genes that can be operably linked to a transcriptional regulatory region responsive to a reconstituted transcriptional activator, and thus used as marker genes (Alam and Cook, 1990, *Anal. Biochem.* 188:245-254).

15 The activation of marker genes like *URA3* or *HIS3* enables the cells to grow in the absence of uracil or histidine, respectively, and hence serves as a selectable marker. Thus, after mating, the cells exhibiting protein-protein interactions are selected by the ability to grow in media lacking a nutritional component, such as uracil or histidine (*see* Le Douarin et al., 1995, *Nucl. Acids Res.* 23:876-878; Durfee et al., 1993, *Genes Dev.* 7:555-569;
20 Pierrat et al., 1992, *Gene* 119:237-245; Wolcott et al., 1966, *Biochem. Biophys. Acta* 122:532-534). In other embodiments of the present invention, the activities of the marker genes like *GFP* or *lacZ* are monitored by measuring a detectable signal (*e.g.*, fluorescent or chromogenic, respectively) that results from the activation of these marker genes. *LacZ* transcription, for example, can be monitored by incubation in the presence of a substrate,
25 such as X-gal (5-bromo-4-chloro-3-indolyl- β -D-galactoside), of its encoded enzyme, β -galactosidase. The pool of all interacting proteins isolated by this manner from mating the *S. cerevisiae* ergosterol-pathway sequence product and the library identifies the "ergosterol-pathway interactive population".

In a preferred embodiment of the present invention, false positives arising
30 from transcriptional activation by the DNA binding domain fusion proteins in the absence of a transcriptional activator domain fusion protein are prevented or reduced by negative selection prior to exposure to the activation domain fusion population (*see e.g.* PCT International Publication No. WO97/47763, published December 18, 1997, which is incorporated by reference herein in its entirety). By way of example, if such cell contains
35 *URA3* as a marker gene, negative selection is carried out by incubating the cell in the presence of 5-fluoroorotic acid (5-FOA, which kills *URA*⁺ cells (Rothstein, 1983, *Meth.*

Enzymol. 101:167-180). Hence, the metabolism of 5-FOA will lead to cell death of self-activating DNA-binding domain hybrids.

In a preferred aspect, negative selection involving a selectable marker as a marker gene can be combined with the use of a toxic or growth inhibitory agent to allow a higher rate of processing than other methods. Negative selection can also be carried out on the activation domain fusion population prior to interaction with the DNA binding domain fusion population, by similar methods, either alone or in addition to negative selection of the DNA binding fusion population. Negative selection can be carried out on the recovered protein-protein complex by known methods (*see e.g.*, Bartel et al., 1993, *BioTechniques* 14:920-924; PCT International Publication No. WO97/47763, published December 18, 1997).

In a preferred embodiment of the invention the DNA sequences encoding the pairs of interactive proteins are isolated by a method wherein either the DNA-binding domain hybrids or the activation domain hybrids are amplified, in separate respective reactions. Preferably, the amplification is carried out by polymerase chain reaction (PCR) (*see* U.S. Patent Nos. 4,683,202; 4,683,195; and 4,889,818; Gyllenstein et al., 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:7652-7656; Ochman et al., 1988, *Genetics* 120:621-623; Loh et al., 1989, *Science* 243:217-220; Innis et al., 1990, *PCR Protocols*, Academic Press, Inc., San Diego, California) using pairs of oligonucleotide primers specific for either the DNA-binding domain hybrids or the activation domain hybrids. Other amplification methods known in the art can be used, including but not limited to ligase chain reaction (*see* EP 320,308), use of Q β replicase, or methods listed in Kricka et al., 1995, *Molecular Probing, Blotting, and Sequencing*, Academic Press, New York, Chapter 1 and Table IX.

The plasmids encoding the DNA-binding domain hybrid and the activation domain hybrid proteins can also be isolated and cloned by any of the methods well known in the art. For example, but not by way of limitation, if a shuttle (yeast to *E. coli*) vector is used to express the fusion proteins, the genes can be recovered by transforming the yeast DNA into *E. coli* and recovering the plasmids from *E. coli* (*see e.g.*, Hoffman et al., 1987, *Gene* 57:267-272). Alternatively, the yeast vector can be isolated, and the insert encoding the fusion protein subcloned into a bacterial expression vector, for growth of the plasmid in *E. coli*.

5.9. BIOCHEMICAL ASSAYS USING REPORTER OR TARGET PROTEINS

The present invention provides for biochemical assays using the reporter or target proteins of the invention. In a specific embodiment, *S. cerevisiae* ergosterol-pathway proteins are useful for biochemical assays aimed at the identification and characterization of

S. cerevisiae substrates or binding partners or the identification of ligands for ergosterol-pathway proteins that are yet to be assigned to the pathway. For any of the reporter or target genes of the invention, the cDNAs encoding reporter or target proteins can be individually subcloned into any of a large variety of eukaryotic expression vectors permitting expression
5 in fungal, yeast, plant, insect, worm, mammalian, or other cell, as described above. The resulting genetically engineered cell lines expressing reporter or target proteins can be assayed for production, processing, and degradation of the reporter or target proteins, for example with antibodies to a specific reporter or target proteins, such as to an *S. cerevisiae* ergosterol-pathway protein, and Western blotting assays, or ELISA assays. For assays of
10 specific binding and functional activation of binding-partner proteins, one can employ either crude culture medium or extracts containing secreted protein from genetically engineered cells (devoid of other ergosterol-pathway proteins), or partially purified culture medium or extracts, or preferably highly purified reporter or target protein fractionated, for example, by chromatographic methods. Alternatively, a reporter or target protein can be synthesized
15 using chemical methods (Nagata, et al., 1992, peptides 13(4):653-62).

Specific protein binding of a reporter or target proteins to the reporter or target binding partners or substrates can be assayed as follows, for example, following the procedures of Yamaguchi et al. (Yamaguchi et al., 1995, *Biochemistry* 34:4962-4968). Chinese hamster ovary cells, COS cells, or any other suitable cell line, can be transiently
20 transfected or stably transformed with expression constructs that direct the production of the reporter or target protein binding-partner or substrate. Direct binding of a reporter or target protein to such binding-partner or substrate-expressing cells can be measured using a "labeled" purified reporter or target protein derivative, where the label is typically a chemical or protein moiety covalently attached to the reporter or target polypeptide which
25 permits the experimental monitoring and quantitation of the labeled reporter or target protein in a complex mixture.

Specifically, the label attached to the reporter or target protein can be a radioactive substituent such as an ^{125}I -moiety or ^{32}P -phosphate moiety, a fluorescent chemical moiety, or labels which allow for indirect methods of detection such as a biotin-
30 moiety for binding by avidin or streptavidin, an epitope-tag such as a Myc- or FLAG-tag, or a protein fusion domain which allows for direct or indirect enzymatic detection such as an alkaline phosphatase-fusion or Fc-fusion domain. Such labeled reporter or target proteins can be used to test for direct and specific binding to binding-partner or substrate-expressing cells by incubating the labeled reporter or target protein with the binding-partner or
35 substrate-expressing cells in serum-free medium, washing the cells with ice-cold phosphate buffered saline to remove unbound reporter or target protein, lysing the cells in buffer with

an appropriate detergent, and measuring label in the lysates to determine the amount of bound reporter or target protein. Alternatively, in place of whole cells, membrane fractions or cell lysates obtained from binding-partner or substrate-expressing cells may also be used. Also, instead of a direct binding assay, a competition binding assay may be used. For
5 example, crude extracts or purified reporter or target protein (such as an *S. cerevisiae* ergosterol-pathway protein) can be used as a competitor for binding of labeled purified reporter or target binding-partner or substrate-expressing cells, by adding increasing concentrations of reporter or target protein to the mixture. The specificity and affinity of binding of the reporter or target protein can be judged by comparison with other reporter or
10 target proteins tested in the same assay.

5.9.1. IDENTIFICATION OF ADDITIONAL BINDING-PARTNERS

The invention described herein provides for methods in which reporter or
15 target proteins are used for the identification of novel reporter or target protein binding-partners, using biochemical methods well known to those skilled in the art for detecting specific protein-protein interactions (Current Protocols in Protein Science, 1998, Coligan et al., eds., John Wiley & Sons, Inc., Somerset, New Jersey). In particular, it is possible that some reporter or target proteins interact with binding-partners that have not yet been
20 discovered, or binding-partners that are specific to a particular organism (*e.g.*, fungi). The identification of either novel binding-partners or specific binding-partners is of great interest with respect to human therapeutic applications, such as, for example, antifungal applications. By way of example, the novel cognate binding-partners for ergosterol-pathway proteins can be investigated and identified as follows. Labeled *S. cerevisiae* ergosterol-
25 pathway proteins can be used for binding assays *in situ* to identify cells possessing cognate binding-partners, for example as described elsewhere (Gorczyca et al., 1993, *J. Neurosci.* 13:3692-3704). Also, labeled *S. cerevisiae* ergosterol-pathway proteins can be used to identify specific binding proteins including binding-partner proteins by affinity chromatography of *S. cerevisiae* protein extracts using resins, beads, or chips with bound *S.*
30 *cerevisiae* ergosterol-pathway protein (Formosa, et al., 1991, *Methods Enzymol* 208:24-45; Formosa, et al., 1983, *Proc. Natl. Acad. Sci. USA* 80(9):2442-6). Further, specific ergosterol-binding proteins can be identified by cross-linking of radioactively-labeled or epitope-tagged ergosterol-pathway protein to specific binding proteins in lysates, followed by electrophoresis to identify and isolate the cross-linked protein species (Ransone, 1995, *Methods Enzymol* 254:491-7). Still further, molecular cloning methods can be used to
35 identify novel binding-partners and binding proteins for *S. cerevisiae* ergosterol-pathway proteins including expression cloning of specific binding-partners using *S. cerevisiae* cDNA

expression libraries transfected into mammalian cells, expression cloning of specific binding proteins using *S. cerevisiae* cDNA libraries expressed in *E. coli* (Cheng and Flanagan, 1994, Cell 79(1):157-68), and yeast two-hybrid methods (as described above) using an *S. cerevisiae* ergosterol-pathway protein fusion as a "bait" for screening activation-domain fusion libraries derived from *S. cerevisiae* cDNA (Young and Davis, 1983, Science 222:778-82; Young and Davis, 1983, Proc. Natl. Acad. Sci. USA 80(5):1194-8; Sikela and Hahn, 1987, Proc. Natl. Acad. Sci. USA 84(9):3038-42; Takemoto, et al., 1997, DNA Cell Biol. 16(6):797-9).

10 5.9.2. ASSAYS OF PATHWAY PROTEINS

The functional activity of reporter or target proteins, derivatives and analogs can be assayed by various methods known to one skilled in the art.

For example, in one embodiment, where one is assaying for the ability to bind to or compete with a wild-type reporter or target protein for binding to an antibody directed to the specific reporter or target protein, various immunoassays known in the art can be used, including but not limited to competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (e.g., using colloidal gold, enzyme or radioisotope labels), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention. In another embodiment, where a reporter or target protein is identified, the binding can be assayed, e.g., by means well-known in the art. In another embodiment, physiological correlates of reporter or target protein binding to its substrates and/or binding-partners (e.g., signal transduction) can be assayed.

In another embodiment, using insect (e.g., Sf9 cells), fly (e.g., *D. melanogaster*), or other model systems (such as other yeast or fungal systems, e.g., *S. pombe*), genetic studies can be done to study the phenotypic effect of a particular reporter or target gene mutant that is a derivative or analog of a wild-type reporter or target gene. Other

such methods will be readily apparent to the skilled artisan and are within the scope of the invention.

The invention provides a method for identifying a molecule that activates the ergosterol pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the ergosterol-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9).

The invention provides a method for identifying a molecule that activates the ergosterol pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the ergosterol-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9).

The invention provides a method for identifying a molecule that activates the PKC pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the PKC-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21).

The invention provides a method for identifying a molecule that activates the PKC pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the PKC-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more

candidate molecules, wherein the reporter gene is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21).

The invention provides a method for identifying a molecule that activates the Invasive Growth pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the Invasive Growth pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

The invention provides a method for identifying a molecule that activates the Invasive Growth pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the Invasive Growth pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

25

5.9.3. PROLIFERATION & CELL CYCLE ASSAYS

A reporter or target gene, such as those of the invention may have potential implications in the ability of a cell to proliferate. The present invention provides for cell cycle and cell proliferation analysis by a variety of techniques known in the art, including but not limited to the following:

Bromodeoxyuridine (BRDU) incorporation may be used as an assay to identify proliferating cells. The BRDU assay identifies a cell population undergoing DNA synthesis by incorporation of BRDU into newly-synthesized DNA. Newly-synthesized DNA may then be detected using an anti-BRDU antibody (*see Hoshino et al.*, 1986, *Int. J. Cancer* 38, 369; *Campana et al.*, 1988, *J. Immunol. Meth.* 107, 79).

Cell Proliferation may also be examined using [³H]-thymidine incorporation *see e.g.*, Chen, J., 1996, *Oncogene* 13:1395-403; Jeoung, J., 1995, *J. Biol. Chem.* 270:18367-73). This assay allows for quantitative characterization of S-phase DNA synthesis. In this assay, cells synthesizing DNA will incorporate [³H]-thymidine into newly synthesized DNA. Incorporation can then be measured by standard techniques in the art such as by counting of radioisotope in a Scintillation counter (*e.g.* Beckman LS 3800 Liquid Scintillation Counter).

Cell proliferation may be measured by the counting samples of a cell population over time (*e.g.* daily cell counts). Cells may be counted using a hemacytometer and light microscopy (*e.g.* HyLite hemacytometer, Hausser Scientific). Cell number may be plotted against time in order to obtain a growth curve for the population of interest. In a preferred embodiment, cells counted by this method are first mixed with the dye Trypan-blue (Sigma), such that living cells exclude the dye, and are counted as viable members of the population. Alternatively, cells in a liquid solution may be counted by absorbency techniques known in the art.

DNA content and/or mitotic index of the cells may be measured, for example, based on the DNA ploidy value of the cell. For example, cells in the G1 phase of the cell cycle generally contain a 2N DNA ploidy value. Cells in which DNA has been replicated but have not progressed thru mitosis (*e.g.* cells in S-phase) will exhibit ploidy value higher than 2N and up to 4N DNA content. Ploidy value and cell cycle kinetics may further be measured using propidium iodide assay (*see e.g.* Turner, T., et al., 1998, *Prostate* 34:175-81). In another embodiment, DNA content may be analyzed by preparation of a chromosomal spread (Zabalou, S., 1994, *Hereditas* 120:127-40; Pardue, 1994, *Meth. Cell Biol.* 44:333-351).

Further assays include but are not limited to detection of changes in length of the cell cycle or speed of cell cycle. In one embodiment the length of the cell cycle is determined by the doubling time of a population of cells. In another embodiment, FACS analysis is used to analyze the phase of cell cycle progression, or purify G1, S, and G2/M fractions (*see e.g.*, Delia, D., et al., 1997, *Oncogene* 14:2137-47). In a further embodiment, length or speed of the cell cycle of a test population is compared to wildtype populations.

Lapse of cell cycle checkpoint(s), and/or induction of cell cycle checkpoint(s), may be examined by the methods described herein, or by any method known in the art. Without limitation, a cell cycle checkpoint is a mechanism which ensures that a certain cellular events occur in a particular order. Checkpoint genes are defined by mutations that allow late events to occur without prior completion of an early event (Weinert, T., and Hartwell, L., 1993, *Genetics*, 134:63-80). Induction or inhibition of cell

cycle checkpoint genes may be assayed, for example, by Western blot analysis, immunostaining, etc. Lapse of cell cycle checkpoints may be further assessed by progression of a cell thru the checkpoint without prior occurrence of specific events (e.g. progression into mitosis without complete replication of the genomic DNA).

5 Other methods will be apparent to one skilled in the art and are within the scope of the invention.

5.9.4. OTHER FUNCTIONAL ASSAYS

For functional assays of a reporter or target protein, beyond substrate binding,
10 the following activities can be investigated using cells expressing a reporter or target protein of the invention after exposing said cells to crude or purified fractions of reporter or target protein and comparing these results with those obtained with other reporter or target proteins described above (Yamaguchi et al., 1995, *Biochemistry* 34:4962-4968). Assayable functional activities include but are not limited to stimulation of cell proliferation; inhibition
15 of cell proliferation; cell death; cell membrane rupture; alterations in cell membrane integrity; stimulation of overall tyrosine kinase activity by immunoblotting of cell extracts with an anti-phosphotyrosine antibody; alteration of specific substrates in the biological-pathway in which the reporter or target are associated and immunoprecipitation with antibodies that specifically recognize the substrate protein; and stimulation of other
20 enzymatic activities linked to the biological-pathway.

5.10. ASSAYS FOR CHANGES IN GENE EXPRESSION

This invention provides assays for detecting changes in the expression of the reporter or target genes and proteins. Assays for changes in gene expression are well known
25 in the art (*see e.g.*, PCT Publication No. WO 96/34099, published October 31, 1996, which is incorporated by reference herein in its entirety). Such assays may be performed *in vitro* using transformed cell lines, immortalized cell lines, or recombinant cell lines, or *in vivo* using animal models.

In particular, the assays may detect the presence of increased or decreased
30 expression of a reporter or target gene or protein on the basis of increased or decreased mRNA expression (using, *e.g.*, nucleic acid probes), increased or decreased levels of related protein products (using, *e.g.*, the antibodies disclosed herein), or increased or decreased levels of expression of a marker gene (*e.g.*, β -galactosidase or luciferase) operably linked to a 5' regulatory region in a recombinant construct.

35 In yet another series of embodiments, various expression analysis techniques may be used to identify genes which are differentially expressed between two conditions,

such as a cell line or animal expressing a normal reporter or target gene compared to another cell line or animal expressing a mutant reporter or target gene. Such techniques comprise any expression analysis technique known to one skilled in the art, including but not limited to differential display, serial analysis of gene expression (SAGE), nucleic acid array
5 technology, subtractive hybridization, proteome analysis and mass-spectrometry of two-dimensional protein gels. In a specific embodiment, nucleic acid array technology (e.g., microarrays) may be used to determine a global (i.e., genome-wide) gene expression pattern in a normal *S. cerevisiae* animal for comparison with an animal having a mutation in one or more *S. cerevisiae* reporter or target genes.

10 To elaborate further, the various methods of gene expression profiling mentioned above can be used to identify other genes (or proteins) that may have a functional relation to (e.g., may participate in a signaling pathway with) a known gene. For example, gene identification of such other genes is made by detecting changes in their expression levels following mutation, i.e., insertion, deletion or substitution in, or overexpression,
15 underexpression, mis-expression or knock-out, of an *S. cerevisiae* ergosterol-pathway gene, as described herein. Expression profiling methods thus provide a powerful approach for analyzing the effects of mutation in an *S. cerevisiae* ergosterol-pathway gene, or any reporter or target gene of the invention.

Methods of gene expression profiling are well-known in the art, as
20 exemplified by the following references describing subtractive hybridization (Wang and Brown, 1991, *Proc. Natl. Acad. Sci. U.S.A.* 88:11505-11509), differential display (Liang and Pardee, 1992, *Science* 257:967-971), SAGE (Velculescu et al., 1995, *Science* 270:484-487), proteome analysis (Humphery-Smith et al., 1997, *Electrophoresis* 18:1217-1242; Dainese et al., 1997, *Electrophoresis* 18:432-442), and hybridization-based methods employing nucleic
25 acid arrays (Heller et al., 1997, *Proc. Natl. Acad. Sci. U.S.A.* 94:2150-2155; Lashkari et al., 1997, *Proc. Natl. Acad. Sci. U.S.A.* 94:13057-13062; Wodicka et al., 1997, *Nature Biotechnol.* 15:1259-1267).

In a preferred specific embodiment of the invention expression analysis techniques are used to identify genes which are differentially expressed upon treatment of a
30 cell with a drug, or by other perturbations. In a further specific embodiment, genes which are co-regulated (e.g., up-regulated upon treatment with a particular drug or antifungal agent) are mapped to gene sets using deletion mutants (See, e.g., Section 6.2) and microarray technology described herein. Still further, labeled cDNAs corresponding to a deletion mutant from drug treated or untreated cells are hybridized to a single microarray.

35

5.11. REPORTER OR TARGET GENE REGULATORY ELEMENTS

This invention provides methods for using reporter or target gene regulatory DNA elements to identify cells, genes, and factors that specifically control reporter or target protein production. In one embodiment, regulatory DNA elements, such as enhancers/promoters, from *S. cerevisiae* ergosterol-pathway genes are useful for identifying and manipulating specific cells that synthesize an ergosterol-pathway protein. Such cells are of considerable interest since they are likely to have an important regulatory function within the fungus in controlling growth, development, reproduction, and/or metabolism. Analyzing components that are specific to a reporter or target secreting cells is likely to lead to an understanding of how to manipulate these regulatory processes, either for therapeutic applications, such as antifungal or fungicide applications, as well as an understanding of how to diagnose dysfunction in these processes. For example, it is of specific interest to investigate whether there are pathways genes in *S. cerevisiae* that might have a function related to that of the mammalian cholesterol pathway in sensing and controlling metabolic activity through the production of an ergosterol-pathway-like protein. Regulatory DNA elements derived from reporter or target genes provide a means to mark and manipulate such cells, and further, identify regulatory genes and proteins, as described below.

5.11.1. PROTEIN-DNA BINDING ASSAYS

In a third embodiment, reporter or target gene regulatory DNA elements are also useful in protein-DNA binding assays to identify gene regulatory proteins that control the expression of such reporter or target genes. Such gene regulatory proteins can be detected using a variety of methods that probe specific protein-DNA interactions well known to those skilled in the art (Kingston, 1998, In *Current Protocols in Molecular Biology*, Ausubel et al, John Wiley & Sons, Inc., sections 12.0.3-12.10) including *in vivo* footprinting assays based on protection of DNA sequences from chemical and enzymatic modification within living or permeabilized cells, *in vitro* footprinting assays based on protection of DNA sequences from chemical or enzymatic modification using protein extracts nitrocellulose filter-binding assays and gel electrophoresis mobility shift assays using radioactively labeled regulatory DNA elements mixed with protein extracts. In particular, it is of interest to identify those DNA binding proteins whose presence or absence is specific to a reporter or target protein as judged by comparison of the DNA-binding assays described above using cells/extracts which express one or more reporter or target gene(s) versus other cells/extracts that do not express the same reporter or target genes. For example, a DNA-binding activity that is specifically present in cells that normally express an ergosterol-pathway protein might function as a transcriptional activator of an ergosterol-pathway reporter or target gene;

conversely, a DNA-binding activity that is specifically absent in cells that normally express an ergosterol-pathway reporter or target protein might function as a transcriptional repressor of the ergosterol-pathway gene. Having identified candidate reporter or target gene regulatory proteins using the above DNA-binding assays, these regulatory proteins can themselves be purified using a combination of conventional and DNA-affinity purification techniques. In this case, the DNA-affinity resins/beads are generated by covalent attachment to the resin of a small synthetic double stranded oligonucleotide corresponding to the recognition site of the DNA binding activity, or a small DNA fragment corresponding to the recognition site of the DNA binding activity, or a DNA segment containing tandemly iterated versions of the recognition site of the DNA binding activity. Alternatively, molecular cloning strategies can be used to identify proteins that specifically bind a reporter or target gene regulatory DNA elements. For example, an *S. cerevisiae* cDNA library in an *E. coli* expression vector, such as the lambda-gt11 vector, can be screened for *S. cerevisiae* cDNAs that encode ergosterol-pathway gene regulatory element DNA-binding activity by probing the library with a labeled DNA fragment, or synthetic oligonucleotide, derived from the ergosterol-pathway gene regulatory DNA, preferably using a DNA region where specific protein binding has already been demonstrated with a protein-DNA binding assay described above (Singh et al., 1989, *Biotechniques* 7:252-61). Similarly, the yeast "one-hybrid" system can be used as another molecular cloning strategy (Li and Herskowitz, 1993, *Science* 262:1870-4; Luo, et al., 1996, *Biotechniques* 20(4):564-8; Vidal, et al., 1996, *Proc. Natl. Acad. Sci. U.S.A.* 93(19):10315-20). In this case, the ergosterol-pathway gene regulatory DNA element, for example, is operably fused as an upstream activating sequence (UAS) to one, or typically more, yeast marker genes such as the *lacZ* gene, the *URA3* gene, the *LEU2* gene, the *HIS3* gene, or the *LYS2* gene, and the marker gene fusion construct(s) inserted into an appropriate yeast host strain. It is expected that in the engineered yeast host strain the reporter genes will not be transcriptionally active, for lack of a transcriptional activator protein to bind the UAS derived from, for example, the *S. cerevisiae* ergosterol-pathway gene regulatory DNA. The engineered yeast host strain can be transformed with a library of *S. cerevisiae* cDNAs inserted in a yeast activation domain fusion protein expression vector, e.g. pGAD, where the coding regions of the *S. cerevisiae* cDNA inserts are fused to a functional yeast activation domain coding segment, such as those derived from the GAL4 or VP16 activators. Transformed yeast cells that acquire *S. cerevisiae* cDNAs that encode proteins that bind the gene regulatory element can be identified based on the concerted activation the marker genes, either by genetic selection for prototrophy (e.g., *LEU2*, *HIS3*, or *LYS2* reporters) or by screening with chromogenic substrates (*lacZ* reporter) by methods known in the art.

6. EXAMPLES

The following examples are provided merely as illustrative of various aspects of the invention and shall not be construed to limit the invention in any way.

5 6.1. **CHARACTERIZATION OF *S. CEREVISIAE* ERGOSTEROL-PATHWAY GENES**

A group of *S. cerevisiae* genes have been discovered as novel reporters of the ergosterol-pathway in the model organism *S. cerevisiae*. This invention provides the following examples of characterization of five *S. cerevisiae* ergosterol-pathway reporter genes described in detail below.

6.1.1. **THE ERGOSTEROL PATHWAY**

Ergosterol is the primary membrane sterol in fungi and in some trypanosomes. Ergosterol serves a structural role comparable to that of cholesterol in mammalian cells, and is essential for the integrity and structure of the fungal cell membrane. As depicted in FIG.9, the ergosterol synthesis pathway contains at least 18 genes designated ERG1 through EGR26. Several different classes of antifungal agents exist which target the ergosterol-pathway.

6.1.2. **CONSTRUCTION OF DELETION MUTANT**

Deletion mutants were constructed by standard techniques, essentially as described by Rothstein, B.,1991, *Meth. Enzymol.* 194:281-301, which is incorporated herein by reference in its entirety. Specifically, a deletion mutant of the entire coding region of YER044C of *S. cerevisiae* was constructed in which the ORF YER044C was replaced by a dominant selectable marker (the kanamycin resistance gene) from *Escherichia coli* (Shoemaker, D. et al.,1996, *Nature Gen.* 14: 450-56; Rothstein, B.,1991, *Meth. Enzymol.* 194:281-301; Baudin, A, et al., 1993, *Nuci. Acids Res.* 21:3329-30). This deletion mutant (R711) has been deposited with Research Genetics (Huntsville, AL) Deletion Consortium Strain #177. Briefly, the bacterial kanamycin resistance cassette (Wach, A et al., 1994, *Yeast* 10:1793-1808) was PCR amplified with primers that added homology to the YER044C locus, to direct homologous integration of the dominant selectable marker. Cell were then transformed with the PCR product. Cell were then selected for G418 resistance, and the gene replacement was confirmed by PCR with the appropriate primers flanking the YER044C locus.

The other genes deletions described in subsections below (e.g., BAR1, FUS3, DIG1, and DIG2) genes were constructed using the same techniques as for YER044C.

6.1.3. GROWTH OF YEAST STRAINS AND DRUG TREATMENT

To assess the effects of pharmacologic inhibition of ergosterol biosynthesis, wild-type *S. cerevisiae* strain R174, (also known as strain BY4741, Brachmann, C., et al, 1998, Yeast, 14(2):115-32) was grown to early log-phase in YPD rich medium at 30°C. The culture was then split into 5 flasks and clotrimazole was added to a cultures at a final concentration of 0.03, 0.1, 1.0, and 3.0 ug/ml. The cultures were then incubated at 30°C for 12 hours. Cells were then harvested, lysed and poly A+ RNA extracted, by methods known in the art. Specifically, cells were harvested and lysed by standard methods (In *Current Protocols in Molecular Biology*, Ausubel et al, John Wiley & Sons, Inc.) with the following modifications: Cell pellets were resuspended in breaking buffer (0.2M Tris HCl, pH 7.6 / 0.5M NaCl / 10mL EDTA / 1% SDS), mixed for 2 minutes on a multi-tube vortex mixer at setting 8 in the presence of 60% (v/v) glass beads (425-600 um mesh; Sigma, St. Louis, MO) and phenol:chloroform (50:50 v/v). Following separation of the phases, the aqueous phase, containing the total RNA, was reextracted and ethanol precipitated. Poly A+ RNA was isolated by two sequential chromatographic purifications over oligo dT cellulose (New England Biololabs Inc, Beverly, MA), as described In *Current Protocols in Molecular Biology*, Ausubel et al, John Wiley & Sons, Inc.

To assess the effects on the ergosterol pathway of deleting the YER044C gene, yeast strains R174 (wild type) and R711 (yer044c::kanR) were grown to early log phase in YPD medium, and harvested for preparation of polyA mRNAs.

6.1.4. PREPARATION AND HYBRIDIZATION OF THE LABELED cDNA

Fluorescentlylabeled cDNA was prepared by reverse transcription of polyA+ RNA in the presence of Cy3- (+ drug) or Cy5- (-drug) deoxynucleotide triphosphates. Fluorescently labeled cDNAs were also purified, and hybridized essentially as described in DeRisi, J., 1997, Science 278:680-86, which is incorporated herein by reference in its entirety. Briefly, Cy3- or Cy5-dUTP (Amersham) was incorporated into cDNA during reverse transcription (Superscript II, Life Technologies, Inc., Gaithersburg, MD). Labeled cDNAs were then concentrated to less than 10 ul using Microcon-30 microconcentrators (Amicon, Millipore, Corp., Bedford, MA). Labeled cDNAs from drug treated or untreated cells were then resuspended in 20-26 ul hybridization solution (3X 55G. 0.75 ug/ml poly A DNA, 0.2% SDS) and applied to the microarray (described below in section 6.2.3) under a 22x30 mm coverslip for 6 h. Both drug treated and untreated samples were simultaneously hybridized to the microarray as described in U.S. Patent serial No. 179,569, filed October 27, 1998 now pending, U.S. Patent serial No. 09/220,275 filed December 23, 1998, now pending, and U.S. Patent serial No. 09/220,142, filed December 23, 1998 now pending,

which are incorporated herein by reference in their entirety. Under these conditions, drug treatment resulted in a signature pattern of altered gene expression in which mRNA levels of about 500 ORFs changed by at least twofold.

Alternatively, fluorescently-labeled cDNA was prepared, as above, by
5 reverse transcription of polyA⁺ RNA from the YER044C deletion mutant and hybridized to the microarray. The signature of the deletion mutant was then compared to the signature of the drug-treated cells, as described below.

6.1.5. FABRICATION OF MICROARRAYS

10 PCR products containing common 5' and 3' sequences were obtained from Research Genetics (Huntsville, AL), and used as templates with amino-modified forward primers and unmodified reverse primers to amplify 6065 ORFs from the yeast genome. Amplification reactions that gave products of unexpected sizes were excluded from
15 subsequent analysis. ORFs that could not be amplified from purchased templates were amplified from genomic DNA. DNA samples from 100 ul reactions were precipitated with isopropanol, resuspended in water, brought up to a total volume of 15 ul in 3X SSC, and transferred to 384-well microtiter plates (Genetix Ltd, Dorset, United Kingdom). PCR
products were robotically spotted onto 1 x 3 inch polylysine-coated glass slides. After printing, slides were processed as described in DeRisi et al. *supra*. 100% of the total ORFs
20 of the yeast genome were amplified and attached to the microarray, thus a DNA microarray consisting of more than 6000 oligonucleotides representing each of the known or predicted ORFs in the yeast genome was prepared.

6.1.6. SCANNING AND IMAGING OF MICROARRAYS

25 Microarrays to which labeled cDNAs had been hybridized were then imaged on a prototype multi-frame charge-coupled device (CCD) camera (Applied Precision, Seattle, WA). Each CCD image frame was approximately 2 mm square. Exposure times of 2 sec in the Cy5 channel (white light through a Chroma 618-648 nm excitation filter, Chroma 657-727 nm emission filter) and 1 sec in the Cy3 channel (Chroma 53 5-560 nm excitation
30 filter, Chroma 570-620 nm emission filter) were taken consecutively in each frame before moving to the next, spatially contiguous frame. Color isolation between the Cy3 and Cy5 channels was 100:1 or better. Frames were knitted together in software to make the complete images as in U.S. Patent serial No. 179,569, filed October 27, 1998 now pending, U.S. Patent serial No. 09/220,275 filed December 23, 1998, now pending, and U.S. Patent serial
35 No. 09/220,142, filed December 23, 1998 now pending, which are incorporated herein by reference in their entirety. The intensity of each spot was quantified from the 10 um pixels

by frame-by-frame background subtraction and intensity averaging in each channel. Normalization between the channels was accomplished by normalizing each channel to the mean intensities of all genes.

5 6.1.7. ASSIGNMENT OF YEAST ORFS TO THE ERGOSTEROL PATHWAY USING DNA MICROARRAY

The ORFs which are the subject of the present invention were discovered to be within the ergosterol pathway using DNA microarray technology (U.S. Patent serial No. 179,569, filed October 27, 1998 now pending, U.S. Patent serial No. 09/220,275 filed
10 December 23, 1998, now pending, and U.S. Patent serial No. 09/220,142, filed December 23, 1998 now pending, which are incorporated herein by reference in their entirety).

Clotrimazole treatment of yeast resulted in the upregulation of approximately 500 genes, many of which were induced by a wide variety of different types of perturbations of yeast. To determine which of these genes specifically associated with the ergosterol-pathway, the clotrimazole transcriptional signatures were compared with many
15 other drug treatments and mutant signatures.

The similarity of signatures was quantified using the correlation coefficient. Correlation coefficients between the signature ORFs of various experiments were calculated according to Equation 4 in section 5.1 above, i.e., by the equation:

$$20 \quad r_{i,j} = \frac{v_i \cdot v_j}{|v_i||v_j|} = \frac{\sum_n (v_i^{(n)} \times v_j^{(n)})}{\left[\sum_n (v_i^{(n)})^2 \sum_n (v_j^{(n)})^2 \right]^{1/2}} \quad (10)$$

25 where $v_i^{(n)}$ and $v_j^{(n)}$ are the \log_{10} of the expression ratio for the genes i and j , respectively, in response to perturbation n . The summation was over those genes that were either up- or down-regulated in either experiment at the 95% confidence level. These genes each had less than a 5% chance of being actually unregulated, that is, having expression ratios departing
30 from unity due to measurement errors alone. This confidence level was assigned based on an error model which assigns a log normal probability distribution to each gene's expression ratio with characteristic width based on the observed scatter in its repeated measurements and on the individual array hybridization quality. This latter dependence was derived from control experiments in which both Cy3 and Cy5 samples were derived from the same RNA
35 sample. As negative controls, deletion mutants known to affect pathways unrelated to ergosterol biosynthesis were analyzed. However, the mutant deleted in YER044C, which

had not previously been assigned any function in the yeast genome, also gave a signature that correlated positively with the signature of drug-treated cells.

Using this analysis, two genes designated YHR039C and YLR100w were discovered to cluster on the same branch (as seen in FIG. 14) and were associated with the ergosterol pathway. These genes have been assigned as reporters of the ergosterol pathway. Three other genes have also been discovered to co-cluster on a second branch (as seen in FIG. 14) and have been discovered to be associated with the ergosterol pathway. These three genes YPL272c, YGR131c, and YDR453c were found to tightly cluster and have therefore been discovered to be associated with the ergosterol-pathway and act as novel reporters for the ergosterol pathway.

Taken together, these data indicated that five *S. cerevisiae* genes, designated YLR100W, YHR039C, YGL001C, YPL272c, YGR131c, and YDR453c were involved in the ergosterol biosynthesis pathway and were novel reporters for the pathway. One or a combination of these genes may also serve as targets for antifungal drug development.

6.2. CHARACTERIZATION OF *S. CEREVISIAE* PKC-PATHWAY GENES

A group of *S. cerevisiae* genes have been discovered as novel reporters and/or targets of the PKC-pathway in the model organism *S. cerevisiae*. This invention provides the following examples of characterization of six *S. cerevisiae* PKC-pathway reporter genes described in detail below. Two of these *S. cerevisiae* PKC-pathway reporter genes have been further validated as target genes and are described in detail below.

6.2.1. THE PKC PATHWAY

Protein kinase C (PKC) is a highly conserved protein throughout all eukaryotes. In the yeast *S. cerevisiae* PKC regulates the (MAP) kinase cascade, which is required for maintenance of cell integrity during periods of asymmetric or polarized growth. FIG. 15 shows a diagram of the PKC pathway in yeast, and demonstrates the reporters and target genes in the PKC pathway that have been discovered by the methods of the invention.

PKC plays a role in regulating the formation of a mating projection. The mating signal is transmitted to PKC through the activities of another Rho-GTPases, CDC42, and BNI1, and RHO1.

6.2.2. NOVEL PKC REPORTER AND TARGET GENES

In order to illustrate the methods of the invention, DNA microarray analysis was used to find reporters and target genes of the PKC pathway. The transcriptional activity of yeast genes across a diverse number of experimental treatments of yeast, including a large

number of drug treatments and mutations, as well as many experiments involving activation of the yeast mating process were used in the clustering analysis methods of the invention. Perturbation of the cells for PKC experiments was performed by constructing constitutively activated alleles of PKC (PKC1-R398A) or RHO1 (RHO-Q68H). Expression of these
 5 alleles were placed under the control of the inducible GAL1/10 promoter, and served as the perturbation. Cells containing constitutively activated alleles of PKC or RHO1 were compared to control cells lacking such activated alleles.

The yeast strains used to find reporter of the PKC pathway as are follows:

10 R4084 = MATa bar1::kanR trp1-63 his3-200 leu2-0 met15-0 ura3-0 pRS316 (CEN URA3)

R4081 = MATa bar1::kanR trp1-63 his 3-200 leu2-0 met15-0 ura3-0 pGAL-RHO1 (GAL1p-RHO1-Q68H, CEN, URA3)

15 R4075 = MATa bar1::kanR leu2-0 his3-1 ura3-0 trp1-63 pGAL-PKC (GAL1p-PKC1-R398A, 2 micron, URA3)

R4081 contained the plasmid pGAL-RHO1, with the RHO1-Q68H gene controlled by the GAL1 promoter, on a low copy CEN, URA3-based plasmid. R4084 was a similar strain,
 20 only contained the plasmid pRS316, which is similar to pGAL-RHO1 except it lacks the RHO1-Q68H gene. R4075 was also similar to R4081, except it contained the plasmid pGAL-PKC, with the PKC1-R398A gene on a high copy 2 micron, URA3-based plasmid.

For PKC experiments, R4084 and R4075 or R4084 and R4081 were grown as pairs of cultures that were treated identically. The strains were grown as overnight cultures
 25 at 30C in SC-ura (synthetic complete medium minus uracil; yeast nitrogen base, ammonium sulfate, and the complete set of amino acid supplements except uracil) with raffinose as the carbon sources. The cells were then subcultured at a low density in fresh medium for 2 hours, then galactose was directly added to the medium at a final concentration of 2%, and incubation continued for 3 hours. The cells were then harvested and total RNAs were
 30 prepared as labeled cDNAs for hybridization to microarrays. Pairs of hybridizations were done for each comparison, with the Cy3 and Cy5 fluors reserved for each pair to eliminate color biases due to differential fluor incorporation, as described above. The competitive hybridization pairs were as follows:

GAL-PKC1-R398A

- 35 1. Cy3=R4084(pRS316) vs Cy5 = R4075 (pGAL-PKC1-R398A)
2. Cy3=R4075 (pGAL-PKC1-R398A) vs Cy5 = R4084 (pRS316)

pGAL-RHO1-Q68H:

1. Cy3=R4084 (pRS316) vs Cy5 = R4081 (pGAL-RHO1-Q68H)
2. Cy3=R4081 (pGAL-RHO1-Q68H) vs Cy5 = R4084 (pRS316)

5 Results of cell perturbation by PKC activated alleles resulted in a large transcriptional response and co-clustered genesets. Comparison of the activated allele experiments to other experiments in the database (e.g., controls) using 2D clustering as described in U.S. Patent serial No. 09/220,275 filed December 23, 1998, now pending, and U.S. Patent serial No. 09/220,142, filed December 23, 1998 now pending, revealed novel
10 reporter genes whose expression is activated only under conditions of PKC activation. These genes included PIR3, YPK2, YLR194C, YDR055W, SLT2 and YKL161C were discovered to be novel reporters of the PKC pathway. These four genes may serve as novel targets for inhibiting or modulating activation of the PKC pathway. Further, two of the genes, SLT2 and YKL161c were found to be located in the PKC pathway, and have
15 therefore been discovered to serve as target genes of the PKC pathway.

Such novel PKC pathway-specific reporters have a wide variety of uses, including for example use in high throughput, cell based assays for general compounds activate PKC. Target genes have a wide variety of uses such as providing a target for which a drug designed to activate, inhibit or modify the PKC pathway may be designed and tested.
20 Such target genes may also serve as the substrate or binding partner for a drug or compound which is tested for activity in activating, inhibiting or modifying the PKC pathway, or cellular responses and phenotypes associated with the PKC pathway, including for example, cell wall integrity.

25 6.3. **CHARACTERIZATION OF *S. CEREVISIAE* INVASIVE GROWTH PATHWAY GENES**

A group of *S. cerevisiae* genes have been discovered as novel reporters and/or targets of the Invasive Growth pathway in the model organism *S. cerevisiae*. This invention provides the following examples of characterization of four *S. cerevisiae* Invasive Growth
30 pathway reporter genes described in detail below. Two of these *S. cerevisiae* pathway reporter genes have been further validated as target genes.

6.3.1. THE INVASIVE GROWTH PATHWAY

The yeast *S. cerevisiae* is dimorphic in that it can either proliferate either by budding or by forming multicellular filaments called pseudohyphae, which can invade the
35 agar (Madhani and Fink, 1998, Trends Cell Biol 1998 Sep;8(9):348-53). Diploid cells undergo the Invasive Growth pathway in response to nitrogen starvation, whereas haploid

cells undergo the Invasive Growth pathway and form invasive filaments on rich medium. The mitogen-activated protein (MAP) kinase cascade is diagramed in FIG. 15.

6.3.2. NOVEL INVASIVE GROWTH REPORTER AND TARGET GENES

5 DNA microarray analysis of the genome of normal and mutant yeast strains was combined with two dimensional (2D) clustering analysis of the behaviors of 6000 genes across many perturbations. Using cluster analysis, a group of genes were identified to be induced transcriptionally in response to perturbations of the Invasive Growth pathway. Genes
10 which were induced specifically to perturbations of the Invasive Growth pathway, were therefore discovered to be reporters for the Invasive Growth pathway. These genes included PGU1, YLR042C, SVS1, and KSS1 gene.

In order to search for Reporter genes of the Invasive Growth pathway, yeast strains with particular mutations (e.g., perturbations) were used as follows. The fus3 strain
15 R500 (MATa bar1::kanR ura3-0 leu2-0 his3-1 met15-0 fus3::URA3) or the dig1 dig2 strain R4063 (MATa bar1::kanR ura3-0 leu2-0 his3-1 met15-0 dig1::LEU2 dig2::URA3), or the isogenic wild type parent, R276 (MATa bar1::kanR ura3-0 leu2-0 his3-1 met15-0), were grown as overnight cultures by standard methods in the art. Each culture was then diluted and grown to log phase. Alpha factor treatment was performed by adding 50 nM alpha
20 factor directly to the cultures and incubating for 30 minutes. The cells were then harvested, total RNA was prepared by standard methods in the art, and polyA mRNAs were selected on oligo-dT cellulose. Next, fluorescently labeled cDNAs were prepared for DNA microarray experiments as described above. The following hybridizations were performed:

- 25 1. Strain R276 (wild type) vs. R500 (fus3), no alpha factor.
2. Strain R276 (wild type) + 50 nM alpha factor, 30 minutes, vs strain R500 (fus3) + 50 nM alpha factor, 30 min.
- 30 3. R276 vs. R4063 (dig1 dig2), neither with alpha factor.

The results of the hybridization experiments were examined by correlating the signatures to the signatures from a wide variety of other experiments, and by cluster analysis of gene behaviors across all these experiments. Four genes were found to be
35 induced specifically in experiments in which the Invasive Growth pathway was activated, including KSS1, PGU1, YLR042C, and SVS1. Surprisingly, the MAPK KSS1 gene serves as a specific reporter and target for experiments in which KSS1 is active.

These target genes provide useful for screening for compounds that block invasive growth in *S. cerevisiae*. Because many aspects of the invasive growth pathway are conserved between *S. cerevisiae* and other pathogenic fungi, such as *Candida albicans*, and the switch to filamentous growth is essential for *C. albicans* virulence, such drugs will
 5 serves as novel antifungal agents.

The KSS1 gene will serve as a useful reporter for activation of the invasive growth pathway, since it has been discovered that induction of this gene is highly specific for this pathway. The use of combinations of two or more of the four invasive growth reporter genes will serve to greatly increase the sensitivity of such a reporter assay.

10 Each of the other genes have been discovered to be induced by other cellular perturbations. Specifically, PGU1 and YLR042C were found to be induced by treatment (e.g., perturbation) with the peptide pheromone, alpha factor. SVS1 was found to be repressed by alpha factor perturbation. Mutants deleted for the DIG1 and DIG2, in the absence of alpha factor, also showed increased transcription of the four genes PGU1,
 15 YLR042C, SVS1, and KSS1. Mutants deleted for the FUS3 MAPK, also showed several fold upregulation of the PGU1, YLR042C, SVS1, and KSS1 genes. Additionally, each of the PGU1, YLR042C, SVS1, and KSS1 genes were induced by activation of KSS1.

Such target genes may also serve as a substrate or binding partner for a drug or compound which is tested for activity in activating, inhibiting or modifying the Invasive
 20 Growth pathway, or cellular responses and phenotypes associated with the Invasive Growth pathway, including for example, invasion of fungus or pathogenicity of fungus.

6.4. NOVEL REPORTER AND TARGET GENES

A group of *S. cerevisiae* genes have been discovered by the methods of the
 25 invention as novel reporters and/or targets of the for pathways in the model organism *S. cerevisiae*. Table I, below lists such genes and there associated pathways, as well as the corresponding SEQ ID NOs.

TABLE I

30	Gene Name	Pathway	FIG.	SEQ ID NO.
	YHR039C	Ergosterol	2	1 DNA
			3	2 Protein
35	YLR100W	Ergosterol	4	3 DNA
			5	4 Protein

	YPL272C	Ergosterol	6	5	DNA
			7	6	Protein
5	YGR131W	Ergosterol	8	7	DNA
			9	8	Protein
	YDR453C	Ergosterol	10	9	DNA
			11	10	Protein
10	SLT2(YHR030C)	PKC	17A-B	11	DNA
			18	12	Protein
	YKL161C	PKC	19A-B	13	DNA
			20	14	Protein
15	PIR3(YKL163W)	PKC	21A-B	15	DNA
			22	16	Protein
20	YPK2(YMR104C)	PKC	23A-B	17	DNA
			24	18	Protein
	YLR194C	PKC	25A-B	19	DNA
			26	20	Protein
25	PST1(YDR055W)	PKC	27A-B	21	DNA
			28	22	Protein
	KSS1(YGR040W)	Invasive Growth	29	23	DNA
			30	24	Protein
30	PGU1(YJR153W)	Invasive Growth	31	25	DNA
			32	26	Protein
35	YLR042C	Invasive Growth	33	27	DNA
			34	28	Protein

SVS1(YPL163C)	Invasive Growth	35	29	DNA
		36	30	Protein

The present invention is not to be limited in scope by the specific
5 embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various references are cited herein above, including patent applications,
10 patents, and publications, the disclosures of which are hereby incorporated by reference in their entireties.

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WHAT IS CLAIMED IS:

1. A method of identifying a reporter gene for a particular biological pathway in a cell comprising identifying a gene which clusters to a geneset associated with the biological pathway, wherein said gene which clusters to the geneset associated with the particular biological pathway is a reporter gene.
2. The method of claim 1, wherein a geneset associated with the particular biological pathway is identified by a method comprising identifying one or more genes in a geneset which are associated with the particular biological pathway, wherein said geneset having one or more genes associated with the particular biological pathway is a geneset associated with the particular biological pathway.
3. The method of claim 1, wherein a geneset associated with the particular biological pathway is identified by identifying a geneset which is activated or inhibited by perturbations which target the biological pathway, wherein a geneset which is activated or inhibited by perturbations which target the biological pathway is a geneset associated with the particular biological pathway.
4. The method of claim 1, further comprising identifying a gene which clusters specifically to a geneset associated with the particular biological pathway, wherein said gene which clusters specifically to the geneset associated with the particular biological pathway is a reporter gene.
5. The method of claim 4, wherein the reporter gene is further identified as a gene whose expression is not altered by perturbations which effect other biological pathways, said other biological pathways being different from said particular biological pathway.
6. The method of claim 1, wherein geneset is provided by a method comprising:
 - (a) measuring changes in expression of a plurality of genes in the cell in response to a plurality of perturbations to the cell; and
 - (b) grouping or re-ordering said plurality of genes into one or more co-varying sets,wherein said one or more co-varying sets comprise said geneset.

7. The method of claim 6, wherein said plurality of genes are grouped or re-ordered into one or more co-varying sets by means of a pattern recognition algorithm.

8. The method of claim 7, wherein the pattern recognition algorithm is a
5 clustering algorithm.

9. The method of claim 8, wherein the clustering algorithm analyzes arrays or matrices, said arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell,
10 wherein said analysis determines dissimilarities between individual genes.

10. The method of claim 6, wherein said plurality of perturbations to the cell are also grouped or re-ordered according to their similarity.

11. The method of claim 10, wherein said plurality of perturbations to the cell are grouped or re-ordered by means of a pattern recognition algorithm.

12. The method of claim 11, wherein the pattern recognition algorithm is a clustering algorithm.
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13. The method of claim 12, wherein the clustering algorithm analyzes arrays or matrices, said arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell.

14. The method of claim 1, wherein the reporter gene is further identified as has a high level of induction.

15. The method of claim 14, wherein expression of the reporter gene is further identified to change by at least a factor of two in response to perturbations of the
30 particular biological pathway.

16. The method of claim 15, wherein expression of the reporter gene is further identified to change by at least a factor of 10 in response to perturbations to the particular biological pathway.
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17. The method of claim 16, wherein expression of the reporter gene is further identified to change by at least a factor of 100 in response to perturbations to the particular biological pathway.

5 18. The method of claim 1, wherein expression of the reporter gene is further identified to change in response to slight perturbations to the particular biological pathway.

10 19. The method of claim 18, wherein the perturbation to the particular biological pathway comprises exposure to a drug, and said reporter gene is further identified to change in response to low levels of exposure to the drug.

20. The method of claim 1, wherein the reporter gene is further identified to respond to perturbations targeted to the entire particular biological pathway.

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21. The method of claim 1, wherein the reporter gene is further identified to respond to perturbations targeted to one or more portions of the particular biological pathway.

20 22. The method of claim 21, wherein the reporter gene is further identified to respond to perturbations targeted to early steps of the particular biological pathway.

25 23. The method of claim 21, wherein the reporter gene is further identified to respond to perturbations targeted to late steps of the particular biological pathway.

24. The method of claim 1, wherein the reporter gene is further identified by identifying a gene which kinetically induces quickly in response to perturbations to the
30 particular biological pathway.

25. The method of claim 24, wherein the reporter gene is further identified by identifying a gene which reaches steady state within about eight hours after a perturbation to the particular biological pathway.

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26. The method of claim 24, wherein the reporter gene is further identified by identifying a gene which reaches steady state within about six hours after a perturbation to the particular biological pathway.

5 27. The method of claim 24, wherein the reporter gene is further identified by identifying a gene which is induced within about two hours after a perturbation to the particular biological pathway.

28. The method of claim 27, wherein the reporter gene is further
10 identified by identifying a gene which is induced within about 90 minutes after a perturbation to the particular biological pathway.

29. The method of claim 28, wherein the reporter gene is further identified by identifying a gene which is induced within about 60 minutes after a
15 perturbation to the particular biological pathway.

30. The method of claim 29, wherein the reporter gene is further identified by identifying a gene which is induced within about 30 minutes after a perturbation to the particular biological pathway.

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31. The method of claim 30, wherein the reporter gene is further identified by identifying a gene which is induced within about 10 minutes after a perturbation to the particular biological pathway.

25 32. The method of claim 31, wherein the reporter gene is further identified by identifying a gene which is induced within about 7 minutes after a perturbation to the particular biological pathway.

30 33. A method of identifying a target gene for a particular biological pathway in a cell comprising identifying a gene which clusters to a geneset associated with the particular biological pathway, wherein said gene which clusters to a geneset associated with the particular biological pathway and is identified as a gene which is necessary for normal function of said particular biological pathway.

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34. The method of claim 33, wherein a geneset associated with the particular biological pathway is identified by a method comprising identifying one or more genes in a geneset which are associated with the particular biological pathway, wherein said geneset having one or more genes associated with the particular biological pathway is a
5 geneset associated with the particular biological pathway.

35. The method of claim 33, wherein a geneset associated with the particular biological pathway is identified by identifying a geneset which is activated or inhibited by perturbations which target the biological pathway, wherein a geneset which is
10 activated or inhibited by perturbations which target the biological pathway is a geneset associated with the particular biological pathway.

36. The method of claim 33, wherein genesets are provided by a method comprising:
15 (a) measuring changes in expression of a plurality of genes in the cell in response to a plurality of perturbations to the cell; and
(b) grouping or re-ordering said plurality of genes into one or more co-varying sets,
wherein said one or more co-varying sets comprise said genesets.

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37. The method of claim 36, wherein said plurality of genes are grouped or re-ordered into one or more co-varying sets by means of a pattern recognition algorithm.

38. The method of claim 37, wherein the pattern recognition algorithm is
25 a clustering algorithm.

39. The method of claim 38, wherein the clustering algorithm analyzes arrays of matrices, said arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell,
30 wherein said analysis determines dissimilarities between individual genes.

40. The method of claim 36, wherein the plurality of perturbations to the cell are also grouped or re-ordered according to their similarity.

35 41. The method of claim 40, wherein the plurality of perturbations to the cell are grouped or re-ordered by means of a pattern recognition algorithm.

42. The method of claim 41, wherein the pattern recognition algorithm is a clustering algorithm.

43. The method of claim 42, wherein the clustering algorithm analyzes
5 arrays of matrices, said arrays or matrices representing said measured changes in expression of the plurality of genes in the cell in response to the plurality of perturbations to the cell.

44. The method of claim 1, wherein the biological pathway is selected from the group consisting of: a signaling pathway, a control pathway, a mating pathway, a
10 cell cycle pathway, a cell division pathway, a cell repair pathway, a small molecule synthesis pathway, a protein synthesis pathway, a DNA synthesis pathway, a RNA synthesis pathway, a DNA repair pathway, a stress-response pathway, a cytoskeletal pathway, a steroid pathway, a receptor-mediated signal transduction pathway, a transcriptional pathway, a translational pathway, an immune response pathway, a heat-shock pathway, a motility
15 pathway, a secretion pathway, an endocytotic pathway, a protein sorting pathway, a phagocytic pathway, a photosynthetic pathway, an excretion pathway, an electrical response pathway, a pressure-response pathway, a protein modification pathway, a small-molecule response pathway, a toxic-molecule response pathway, and a transformation pathway.

20 45. The method of claim 1, wherein the reporter gene is a reporter for the ergosterol-pathway, and the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as
25 depicted in FIG.10, as set forth in SEQ ID NO:9).

46. The method of claim 1, wherein the reporter gene is a reporter for the PKC-pathway, and the reporter gene is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as
30 depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21).

35 47. The method of claim 33, wherein the biological pathway is selected from the group consisting of: a signaling pathway, a control pathway, a mating pathway, a

cell cycle pathway, a cell division pathway, a cell repair pathway, a small molecule synthesis pathway, a protein synthesis pathway, a DNA synthesis pathway, a RNA synthesis pathway, a DNA repair pathway, a stress-response pathway, a cytoskeletal pathway, a steroid pathway, a receptor-mediated signal transduction pathway, a transcriptional pathway, a translational pathway, an immune response pathway, a heat-shock pathway, a motility pathway, a secretion pathway, an endocytotic pathway, a protein sorting pathway, a phagocytic pathway, a photosynthetic pathway, an excretion pathway, an electrical response pathway, a pressure-response pathway, a protein modification pathway, a small-molecule response pathway, a toxic-molecule response pathway, and a transformation pathway.

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48. The method of claim 33, wherein the target gene of the PKC-pathway is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), and YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13).

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49. A method for determining whether a molecule affects the function or activity of an ergosterol pathway in a cell comprising:

- (a) contacting the cell with, or recombinantly expressing within a cell the molecule; and
- (b) determining whether the expression of one or more of the genes selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9) is changed relative to said expression in the absence of the molecule.

25

50. The method according to claim 49 which is a method for determining whether the molecule inhibits ergosterol synthesis such that a cell contacted with the molecule exhibits a lower level of ergosterol than a cell which is not contacted with said molecule.

51. The method according to claim 49 wherein step (b) comprises determining whether YPL272c expression increases.

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52. A kit comprising in one or more containers a) a substance selected from the group consisting of an antibody against an ergosterol-pathway protein, a gene probe capable of hybridizing to RNA of an ergosterol-pathway gene, and pairs of gene primers capable of priming amplification of at least a portion of an ergosterol-pathway gene, and b) a molecule known to be capable of perturbing the ergosterol pathway.

53. A method for identifying a molecule that activates the ergosterol pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the ergosterol-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9).

54. A method for identifying a molecule that activates the ergosterol pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the ergosterol-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9).

55. The method according to claim 53, wherein the fungal cell is a transgenic cell.

56. The method according to claim 54, wherein the fungal cell is a transgenic cell.

57. A method for identifying a molecule that modulates the expression of an ergosterol-pathway gene selected from the group consisting of YHR039C (as depicted in FIG.2, as set forth in SEQ ID NO:1), YLW100W (as depicted in FIG.4, as set forth in SEQ ID NO:3), YPL272C (as depicted in FIG.6, as set forth in SEQ ID NO:5), YGR131W (as

depicted in FIG.8, as set forth in SEQ ID NO:7), and YDR453C (as depicted in FIG.10, as set forth in SEQ ID NO:9); comprising recombinantly expressing in a fungal cell one or more candidate molecules, and detecting the expression of said ergosterol-pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates ergosterol-pathway gene expression.

58. The method according to claim 57, wherein the fungal cell is a transgenic cell.

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59. A method for identifying a molecule that modulates the activity of an ergosterol-pathway protein selected from the group consisting of YHR039C (as depicted in FIG.3, as set forth in SEQ ID NO:2), YLW100W (as depicted in FIG.5, as set forth in SEQ ID NO:4), YPL272C (as depicted in FIG.7, as set forth in SEQ ID NO:6), YGR131W (as depicted in FIG.9, as set forth in SEQ ID NO:8), and YDR453C (as depicted in FIG.11, as set forth in SEQ ID NO:10), comprising contacting a fungal cell with one or more candidate molecules, detecting said protein; wherein an increase or decrease in the protein level relative to the level in the absence of candidate molecules indicates that the molecule modulates ergosterol-pathway gene expression.

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60. A method of identifying a molecule that binds to a ligand selected from the group consisting of (i) an *S. cerevisiae* ergosterol-pathway protein selected from the group consisting of YHR039C (as depicted in FIG.3, as set forth in SEQ ID NO:2), YLW100W (as depicted in FIG.5, as set forth in SEQ ID NO:4), YPL272C (as depicted in FIG.7, as set forth in SEQ ID NO:6), YGR131W (as depicted in FIG.9, as set forth in SEQ ID NO:8), and YDR453C (as depicted in FIG.11, as set forth in SEQ ID NO:10), (ii) a fragment of the *S. cerevisiae* ergosterol-pathway protein, and (iii) a nucleic acid encoding the *S. cerevisiae* ergosterol-pathway protein or fragment, the method comprising:

- 30 (a) contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and
(b) identifying a molecule within the plurality that binds to the ligand.

61. A method for determining whether a molecule affects the function or activity of an PKC pathway in a cell comprising:

- 35 (a) contacting the cell with, or recombinantly expressing within a cell the molecule; and

- 5 (b) determining whether the expression of one or more of the genes selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21) is changed relative to said expression in the absence of the molecule.
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62. The method according to claim 61 wherein step (b) comprises determining whether SLT2 expression increases.

- 15 63. A kit comprising in one or more containers a) a substance selected from the group consisting of an antibody against a PKC-pathway protein, a gene probe capable of hybridizing to RNA of a PKC-pathway gene, and pairs of gene primers capable of priming amplification of at least a portion of a PKC-pathway gene, and b) a molecule known to be capable of perturbing the PKC pathway.

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64. A method for identifying a molecule that activates the PKC pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the PKC-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of: SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21).
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- 30

65. A method for identifying a molecule that activates the PKC pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the PKC-pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the group consisting of:
- 35

SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21)

66. The method according to claim 64, wherein the fungal cell is a transgenic cell.

67. The method according to claim 65, wherein the fungal cell is a transgenic cell.

68. A method for identifying a molecule that modulates the expression of a PKC-pathway gene selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.17A-B, as set forth in SEQ ID NO:11), YKR161C (as depicted in FIG.19A-B, as set forth in SEQ ID NO:13), PIR3(YKL163W) (as depicted in FIG.21A-B, as set forth in SEQ ID NO:15), YPK2(YMR104C) (as depicted in FIG.23A-B, as set forth in SEQ ID NO:17), YLR194C (as depicted in FIG.25A-B, as set forth in SEQ ID NO:19), and ST1(YDR055W) (as depicted in FIG.27A-B, as set forth in SEQ ID NO:21), comprising recombinantly expressing in a fungal cell one or more candidate molecules, and detecting the expression of said PKC-pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates PKC-pathway gene expression.

69. The method according to claim 68, wherein the fungal cell is a transgenic cell.

70. A method for identifying a molecule that modulates the activity of a PKC-pathway protein selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.18, as set forth in SEQ ID NO:12), YKR161C (as depicted in FIG.20, as set forth in SEQ ID NO:14), PIR3(YKL163W) (as depicted in FIG.22, as set forth in SEQ ID NO:16), YPK2(YMR104C) (as depicted in FIG.24, as set forth in SEQ ID NO:18), YLR194C (as depicted in FIG.26, as set forth in SEQ ID NO:20), and ST1(YDR055W) (as depicted in FIG.28, as set forth in SEQ ID NO:22), comprising contacting a fungal cell with one or more candidate molecules, detecting said protein; wherein an increase or decrease in the protein

level relative to the level in the absence of candidate molecules indicates that the molecule modulates PKC-pathway gene expression.

71. A method of identifying a molecule that binds to a ligand selected
5 from the group consisting of (i) an *S. cerevisiae* PKC-pathway protein selected from the group consisting of SLT2(YHR030C) (as depicted in FIG.18, as set forth in SEQ ID NO:12), YKR161C (as depicted in FIG.20, as set forth in SEQ ID NO:14), PIR3(YKL163W) (as depicted in FIG.22, as set forth in SEQ ID NO:16), YPK2(YMR104C) (as depicted in FIG.24, as set forth in SEQ ID NO:18), YLR194C (as depicted in FIG.26, as
10 set forth in SEQ ID NO:20), and ST1(YDR055W) (as depicted in FIG.28, as set forth in SEQ ID NO:22), (ii) a fragment of the *S. cerevisiae* PKC-pathway protein, and (iii) a nucleic acid encoding the *S. cerevisiae* PKC-pathway protein or fragment, the method comprising:
- (a) contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and
 - 15 (b) identifying a molecule within the plurality that binds to the ligand.

72. A method for determining whether a molecule affects the function or activity of an Invasive Growth pathway in a cell comprising:
- 20 (a) contacting the cell with, or recombinantly expressing within a cell the molecule; and
 - (b) determining whether the expression of one or more of the genes selected from the group consisting of: KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as
25 depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29), is changed relative to said expression in the absence of the molecule.

73. The method according to claim 72 wherein step (b) comprises determining whether KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), expression increases.
- 30

74. A kit comprising in one or more containers a) a substance selected
35 from the group consisting of an antibody against an Invasive Growth pathway protein, a gene probe capable of hybridizing to RNA of an Invasive Growth pathway gene, and pairs of

gene primers capable of priming amplification of at least a portion of an Invasive Growth pathway gene, and b) a molecule known to be capable of perturbing the Invasive Growth pathway.

5 75. A method for identifying a molecule that activates the Invasive Growth pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the RNA expression of a reporter gene for the Invasive Growth pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected from the
10 group consisting of KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

15 76. A method for identifying a molecule that activates the Invasive Growth pathway in yeast comprising contacting a yeast cell with one or more candidate molecules, and detecting a change in the protein expression of a reporter gene for the Invasive Growth pathway relative to the expression of the reporter gene in a yeast cell not contacted by the one or more candidate molecules, wherein the reporter gene is selected
20 from the group consisting of: KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

25 77. The method according to claim 75, wherein the fungal cell is a transgenic cell.

 78. The method according to claim 76, wherein the fungal cell is a transgenic cell.

30 79. A method for identifying a molecule that modulates the expression of an Invasive Growth pathway gene selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as depicted in FIG.33, as set forth in
35 SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29), comprising recombinantly expressing in a fungal cell one or more candidate

molecules, and detecting the expression of said Invasive Growth pathway gene; wherein an increase or decrease in the gene expression relative to the expression in the absence of candidate molecules indicates that the molecules modulates Invasive Growth pathway gene expression.

5

80. The method according to claim 79, wherein the fungal cell is a transgenic cell.

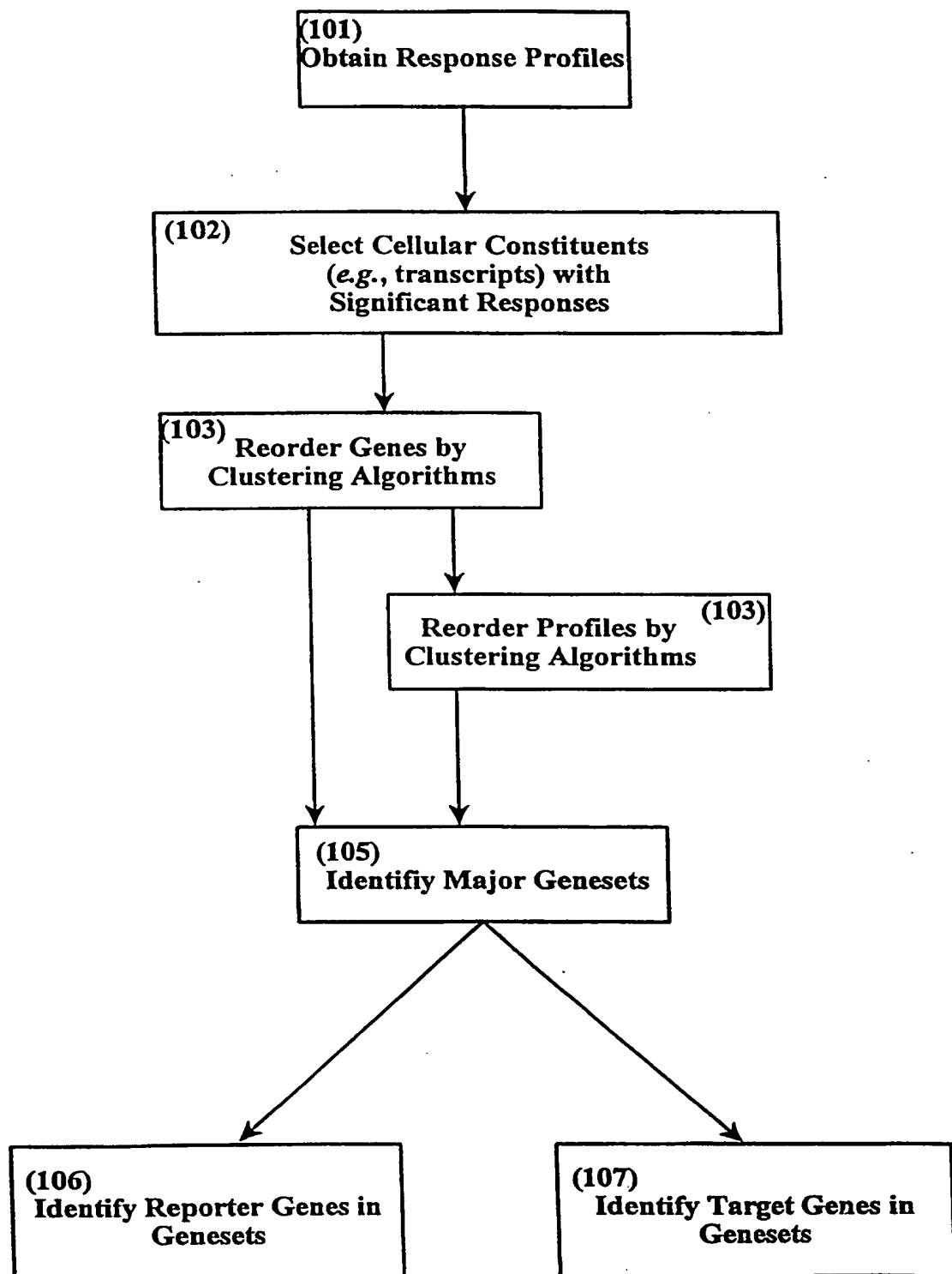
81. A method for identifying a molecule that modulates the activity of an
10 Invasive Growth pathway protein selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.30, as set forth in SEQ ID NO:24), PGU1(YJR153W) (as depicted in FIG.32, as set forth in SEQ ID NO:26), YRL042C (as depicted in FIG.34, as set forth in SEQ ID NO:28), and SVS1(YPL163C) (as depicted in FIG.36, as set forth in SEQ ID NO:30), comprising contacting a fungal cell with one or more candidate molecules,
15 detecting said protein; wherein an increase or decrease in the protein level relative to the level in the absence of candidate molecules indicates that the molecule modulates Invasive Growth pathway gene expression.

82. A method of identifying a molecule that binds to a ligand selected
20 from the group consisting of (i) an *S. cerevisiae* Invasive Growth pathway protein selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.30, as set forth in SEQ ID NO:24), PGU1(YJR153W) (as depicted in FIG.32, as set forth in SEQ ID NO:26), YRL042C (as depicted in FIG.34, as set forth in SEQ ID NO:28), and SVS1(YPL163C) (as depicted in FIG.36, as set forth in SEQ ID NO:30), (ii) a fragment of the *S. cerevisiae*
25 Invasive Growth pathway protein, and (iii) a nucleic acid encoding the *S. cerevisiae* Invasive Growth pathway protein or fragment, the method comprising:

- (a) contacting the ligand with a plurality of molecules under conditions conducive to binding between the ligand and the molecules; and
- (b) identifying a molecule within the plurality that binds to the ligand.

30

83. The method of claim 1, wherein the reporter gene is a reporter for the Invasive Growth pathway, and the reporter gene selected from the group consisting of KSS1(YGR040W) (as depicted in FIG.29, as set forth in SEQ ID NO:23), PGU1(YJR153W) (as depicted in FIG.31, as set forth in SEQ ID NO:25), YRL042C (as
35 depicted in FIG.33, as set forth in SEQ ID NO:27), and SVS1(YPL163C) (as depicted in FIG.35, as set forth in SEQ ID NO:29).

**FIG. 1**

YHR039C DNA sequence, including the coding region, 350 bp of upstream sequence, and 100 bp of downstream sequence.

```

TCTAGTTTTT TAATCATATA TCTTTTTTATA ATATAATACC AATAGAATAA 51
AAATGTATAA ACTGACATTG CATTGCGTCT TTACGACTCT CGCTTTATCC 101
ATTCAGCCTT TTTTTTTTTT TTTTTTTTTT CTCTATCTGC TAAACGAGTA 151
GTAGTATAAT CAAAATGTG TTATTTAGTA TATCGGTTGT AAAGGAGAAA 201
GTATGGTCTC TCTATTTTAA TTTTATTAAC GAAAAATACT AAACGCCGAT 251
GGGGATTACT ATATAATTAT AATAGTATTT GCAGAATAGT AGAATTCCTT 301
TCACAGTTCA CGTTCAGTTT CTCCTCTGTT TTATCGAACG TTTATTCATC 351

ATGTCCAAGG TCTATCTGAA TTCAGACATG ATTAACCATT TGAACTCCAC 401
AGTTCAAGCT TACTTTAACT TATGGTTGGA GAAGCAAAAC GCAATAATGC 451
GTTCTCAACC CCAAATTATT CAAGATAACC AAAAAGTATG AGGCATTACA 501
ACGCTAGTTG CCTCAATTTT CACTCTGTAT GTTTTGGTCA AGATAATCTC 551
CACCCAGCA GAGTGTTCCT CGTCCTATAA GCCAGTCAA TTCTCCCTTC 601
CTGCACCAGA GGCCGCTCAA AATAATTGGA AGGGCAAGAG GTCTGTTTCC 651
ACTAACATAT GGAATCCTGA AGAACCAAAC TTTATTCAT GTCATTTGCC 701
CGCCACAGGT CAATATCTAG GTTCTTTTCC ATCGAAAACG GAAGCTGACA 751
TAGATGAAAT GGTTCCTAAG GCAGGCAAAG CTCAATCTAC TTGGGGCAAT 801
TCTGATTTCT CAAGAAGATT GAGAGTTTGT GCTTCTTTGC ATGATTATAT 851
TCTAAATAAT CAAGATCTTA TTGCGAGAGT AGCGTGCAGG GATTCAGGAA 901
AGACAATGTT AGACGCATCG ATGGGTGAAA TCTTGTTTAC TTTAGAAAAA 951
ATTCAATGGA CTATAAAGCA CGGCCAAAGA GCGTTGCAAC CTTGAGACG 1001
TCCGGGCCCC ACTAATTTT TCATGAAGTG GTATAAAGGT GCAGAAATCC 1051
GTTATGAACC ACTGGGTGTG ATCAGTTCTA TCGTTTCCTG GAACTATCCA 1101
TTCCATAACT TATTGGGTCC AATTATTGCA GCATTGTTCA CAGGGAATGC 1151
CATTGTAAGT AAATGTTTCA AACAAGTTGT CTGGTCTTCG GAATTTTTCG 1201
TCGAGCTGAT CCGCAAATGT TTGGAAGCTT GTGATGAAGA TCCGATTTG 1251
GTTCAAGTTG GCTATTGTTT ACCTCCAAC GAAATGATG ATTCCGCAAA 1301
TTATTTTACC TCTCATCCTG GTTTCAAACA TATCACTTTT ATTGGCAGTC 1351
AGCCCGTAGC GCACTATATT CTAAAATGCG CTGCCAAATC ATTGACACCC 1401
GTAGTTGTGG AGCTTGGTGG TAAGGATGCG TTTATTGTCC TAGACTCAGC 1451
TAAGAATTTA GATGCTTTAT CTTCTATCAT CATGAGGGGT ACTTTCCAAT 1501
CATCCGGTCA AAATGTGATT GGTATTGAGA GGGTTATTGT CAGTAAGGAA 1551
AATTATGATG ATTTAGTCAA GATTTTGAAT GACCGTATGA CTGCAATCC 1601
ACTACGCCAA GGGTCTGATA TTGATCATTT AGAAAATGTT GATATGGGGG 1651
CAATGATATC TGACAACAGA TTCGATGAAC TAGAAGCTTT GGTAAAGAT 1701
GCTGTTGCAA AGGGAGCTCG TTTACTTCAA GGTGGTTCCC GCTTCAAACA 1751
TCCAAAGTAT CCACAAGGTC ATTATTTCCA ACCAACTCTT TTGGTGGATG 1801
TCACTCCAGA AATGAAAATA GCACAAAACG AAGTGTTTGG CCAATTTTA 1851
GTCATGATGA AAGCTAAGAA TACTGACCAT TGTGTACAAC TAGCCAACTC 1901
TGCGCCATTT GGTCTAGGTG GTTCTGTGTT TGGTGCGGAT ATCAAGGAAT 1951
GCAATTACGT CGCAAATAGC CTACAAACTG GTAATGTAGC CATTAAATGAT 2001
TTTGCTACAT TCTATGTTTG TCAATTACCA TTTGGTGGTA TCAATGGTTC 2051
AGGTACGGT AAATTTGGTG GTGAAGAAGG TCTTTTGGGT TTGTGCAATG 2101
CCAAAAGTGT CTGTTTGGAT ACTTTGCCCT TTGTCTCCAC TCAAATTTCCA 2151
AAACCATTAG ACTACCCTAT TCGTAACAAAT GCTAAGGCTT GGAATTTTGT 2201
AAAGAGTTTC ATCGTAGGAG CTTATACAAA TTCCACATGG CAAAGAATAA 2251
AGTCACTGTT CTCTTTAGCT AAAGAAGCCA GCTAG

TTTAC TTTAGAGGAA 2301
GCAACAACT TATCAATAAT TTGGTATTTA TTATTATATA AAATGAACTT 2351
TTTATGTACA AGATTTATGA TTTTTTGATT CTATA

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FIG. 2

Yhr039c protein sequence.

MSKVYLNSDMINHLNSTVQAYFNLWLEKQNAIMRSQPQIIQDNQKLIGITTLLVASIFTLY
VLVKIISTPAKCSSSYKPVKFSLPAPEAAQNNWKGKRSVSTNIWNPEEPNFIQCHCPATG
QYLGSFPSKTEADIDEMVSKAGKAQSTWGNPDFSRRLRVLASLHDYILNNQDLIARVACR
DSGKTMLDASMGEILVTLEKIQWTIKHGQRALQPSRRPGPTNFFMKWYKGAEIRYEPLGV
ISSIVSWNYPFHNLLGPIIAALFTGNAIVVKCSEQVVSSEFFVELIRKCLEACDED PDL
VQLCYCLPPTENDDSANYFTSHPGFKHITFIGSQPVAHYILKCAAKSLTPVVVELGGKDA
FIVLDSAKNLDALSSIIMRGTFQSSGQNCIGIERVIVSKENYDDLVLKILNDRMTANPLRQ
GSDIDHLENVDMGAMISDNRFDELEALVKDAVAKGARLLQGGSRFKHPKYPOGHYFQPTL
LVDVTPEMKIAQNEVFGPIILVMMKAKNTDHCVQLANSAPFGLGGSVFGADIKCNYVANS
LQTGNVAINDFATFYVCQLPFGGINGSGYGKFGGEEGLLGLCNAKSVCFDTLPFVSTQIP
KPLDYPIRNNAKAWNFVKSFIVGAYTNSTWQRIKSLFSLAKEAS

FIG. 3

YLR100W DNA Sequence, including the coding sequence
(with the start and stop codons in bold), plus 800 bp of upstream
sequence and 100 bp of downstream sequence.

```

ACGTACAAAA AAGAGCACGC TGCTTTATTT ATACTTTTGT GCCACAAGAA 51
TGATCAACAT CAACATAAAT ATCAACTAGT ATCTGCAACA CATCTGCTCC 101
ACGGAACATA ACCCGTTGAG CAGTGCCCCG TGGAAACGTA AACTATCGCA 151
AATTGGGATT AACAAGCCAA AAACAGCCAA GCAAGATTCA CGAAACCGCG 201
CCTCGTTTGG ACCCCGAAGG CCCATTTAAC GGCCGGCCGT TACAAGCAAG 251
ATCGGCAGAG CAAACCACTC CCCAGCACCA CAGCACATCA CTGCACGAGC 301
AACATAAAT AGAACATGGC AGATAGCGAG GATACCTCTG TGATCCTGCA 351
GGGCATCGAC ACAATCAACA GCGTGGAGGG CCTGGAAGAA GATGGTTACC 401
TCAGCGACGA GGACACGTCA CTCAGCAACG AGCTCGCAGA TGCACAGCGT 451
CAATGGGAAG AGTCGCTGCA ACAGTTGAAC AAGCTGCTCA ACTGGGTCTT 501
GCTGCCCCTG CTGGGCAAGT ATATAGGTAG GAGAATGGCC AAGACTCTAT 551
GGAGTAGGTT CATTGAACAC TTTGTATAAG TGTTTGTTGT TTATGTATCC 601
GCATATAGCA GTTATAACAG ATAAATGGCA CTTTTCGCAC ACCCGTTGTT 651
TTATCTCCGA TAGTACGTGG GCCTTTATTT ATGGTCGTTT AACGAAAGAA 701
CGGCATCTTG AATTGAGCAG GTATTTAAAA GATAGGACGA GAAACAAGCA 751
CATGATCTGT GTCGAAAAAA AGTAGCAAAG AGAAAAAGTA GGAGGATAGG 801

ATGAACAGGA AAGTAGCTAT CGTAACGGGT ACTAATAGTA ATCTTGGTCT 851
GAACATTGTG TTCCGTCTGA TTGAAACTGA GGACACCAAT GTCAGATTGA 901
CCATTGTGGT GACTTCTAGA ACGCTTCCTC GAGTGCAGGA GGTGATTAAC 951
CAGATTAAAG ATTTTACAA CAAATCAGGC CGTGTAGAGG ATTTGGAAAT 1001
AGACTTTGAT TATCTGTTGG TGGACTTCAC CAACATGGTG AGTGCTCTGA 1051
ACGCATATTA CGACATCAAC AAAAAGTACA GGGCGATAAA CTACCTTTTC 1101
GTGAATGCTG CGCAAGGTAT CTTTGACGGT ATAGATTGGA TCGGAGCGGT 1151
CAAGGAGGTT TTCACCAATC CATTGGAGGC AGTGACAAAT CCGACATACA 1201
AGATACAACT GGTGGGCGTC AAGTCTAAAG ATGACATGGG GCTTATTTTC 1251
CAGGCCAATG TGTTTGGTCC GTACTACTTT ATCAGTAAAA TTCTGCCTCA 1301
ATTGACCAGG GGAAAGGCTT ATATTGTTTG GATTTCGAGT ATTATGTCCG 1351
ATCCTAAGTA TCTTTCGTTG AACGATATTG AACTACTAAA GACAAATGCC 1401
TCTTATGAGG GCTCCAAGCG TTTAGTTGAT TTACTGCATT TGGCCACCTA 1451
CAAAGACTTG AAAAAGCTGG GCATAAATCA GTATGTAGTT CAACCGGGCA 1501
TATTTACAAG CCATTCCTTC TCCGAATATT TGAATTTTTT CACCTATTTT 1551
GGCATGCTAT GCTTGTCTTA TTTGGCCAGG CTGTTGGGGT CTCCATGGCA 1601
CAATATTGAT GGTATATAAG CTGCCAATGC CCCAGTATAC GTAAGTAGAT 1651
TGGCCAATCC AAACCTTGAG AAACAAGACG TAAAATACGG TTCTGCTACC 1701
TCTAGGGATG GTATGCCATA TATCAAGACG CAGGAAATAG ACCCTACTGG 1751
AATGTCTGAT GTCTTCGCTT ATATACAGAA GAAGAAACTG GAATGGGACG 1801
AGAAACTGAA AGATCAAATT GTTGAAACTA GAACCCCAT TTAATATC 1851
TCTGCGTACA TATGTATATA TATATATGTG TGTATATACA TGTATGTCTG 1901
TAGAGAAAC GCATATCAAC TGATATATAT ACACGTGAAG CAAATATC

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FIG. 4

Ylr100w protein sequence.

MNRKVAIVTGTNSNLGLNIVFRLIETEDTNVRLTIVVTSRTLPRVQEVINQIKDFYNKSG
RVEDLEIDFDYLLVDFTNMVSVLNAYYDINKKYRAINYL FVNAAQGIFDGIDWIGAVKEV
FTNPLEAVTNPTYKIQLVGVKSKDDMGLIFQANVFGPYFFISKILPQLTRGKAYIVWISS
IMSDPKYLSLNDIELLKTNASYEGSKRLVDLLHLATYKDLKKLGINQYVVPQPGIFTSHSF
SEYLNFFTYFGMLCLFYLARLLGSPWHNIDGYKAANAPVYVTRLANPNFEKQDVKYGSAT
SRDGMPYIKTQEIDPTGMSDVFAYIQKKLEWDEKLKDQIVETRTPI

FIG. 5

YPL272c DNA sequence

```

1      GATGGCAAAC CTCCGCAATG ATTGGCGTTC TAGCGGCTAT CCGAATTCAC
51     AATCGACAAG AAGTACTTCT AACTTACACA AGGCAACGAA ATAATATCAC
101    TCTATGAAAC TGCCATTTGG GTAATAGGAG TATATTGAAC GACACCGGGT
151    CAACAAGCAA CTTTCCTAAG CCTTTTACAC TTCTTCACAT CATTCAAGAT
201    CGCCTTTTAA CGAGCTACAA ACCTTCACGT TCGTTCCTCT ATGGAAACGT
251    TTAAGATAAC GTTAAAACGT TCTCAATCAC AGAATTTAAG ATGATTAGAA
301    ATGTTTTCCTA AGGGATAGGG CGAAGCACAA CCTCGAAAAA TGGCAAAATT
351    TTAGAATCTT AGCCACCTTA ACGTCTACTT AGAGCCTTAG AAAAGCCATC
401    AAGATTGGTG GAATAGTTGT TGAGGGAAC TTAGCCGCCAC ATTCTCGTAG
451    CCAAATAAAG CGAATCTGAC CATTGTATGT TTCTTTTTTCA CTGGTATGAT
501    AGCCCAATGT GTTTAAGGAA AGTTAGGACA ACACACCCGA AGAAGGACGT
551    CACCCCTGCA TTCCCAAACG AGCTATGAAA TAGCTCTTTC CTCTACAAGT
601    AATAACAACA ACTTTTTTGT CTGTTTCCG ACCGTTTAAC TTCAGAGATT
651    AATTTTTTCA ACGCGCTTTC GTTGAACGTC GCAAATTCGT TTAGAATAAA
701    CGAAAGGTGA CAGAAATAGA AGATTATAGC CATGCATACG CACATAAATT
751    GAAAACGTGT TCGAGGCTGA GTATTCCCTG CGTCTGCAGC CATCAGGGGT
801    ATGACTCTGC TACACGTTTA CTATATTCTT GGCTAAACGA TTCATTAACG
851    AAGCGATGAG TAGATCACAC TCGGCATACG AGCACAAATT TGTATGGGGG
901    GACGGTCATA TATAAAAGGG TGTATACGTT ATCCTTGTTA TACCTGTCCA
951    AAGAAGTGCA TTTGTAAC TCACAACAGA CACATCCTCA CTTTATCATA

1001   ATGACTACGT TTAGGCCACT ATCAAGTTTT GAAAAAATAA TTCTCACTCA
1051   ATCTTTGAAT GACCAAAGAA ATGGAACAT TTTTTCGAGT ACATATTCAA
1101   AATCTTTAAG TAGAGAAAAA GACGCTGACT GGCATTCTGA TGAATCTACG
1151   CTCGGAACAA ATTCTTCCAA AGATGATTCT CGTCTGACTC TGCCCTCAAT
1201   AGCAACAAC TTTGAAGAGAT TGATTAAATC GCAACCGGCA TTGTTTGCAA
1251   CTGTAAACGA AGAATGGGAA TTCGAGCCAT TGAAGCAGCT GAAAACCTCC
1301   GATATTGTTA ATGTGATTGA GTTTGAAACC ATAAAAGATA AGGAGGTCAA
1351   TTGCCATTGG GGTGTTCCAC CTCCTTATCT CTTGCGTCAT GCCTTCAACA
1401   AGACTAGATT TGTTCCCGGA TCAAATAAAC CTTTATGGAC ACTATATGTA
1451   ATTGACGAAG CGCTATTGGT TTTTCATGGT CACGACGTAT TGTTTGATAT
1501   ATTTTCAGCA GCTAACTTTC ACAAAATTAT TTTAAAAGAG TTAAACGAAA
1551   TCAGCACAGT AACACACTCT GAAGATAGGA TTTTGTTTGA TGTCAATGAC
1601   ATCAATCTCT CAGAATTAAA ATTTCCCAAA TCGATATATG ATAGCGCAAA
1651   ATTACACCTG CCCGCTATGA CACCACAAAT CTTCCACAAG CAAACTCAGT
1701   CATTTTTCAA ATCAATATAC TATAACACTT TAAAAAGACC TTTCCGGCTAT
1751   TTAACCAATC AAACCTCCCT CAGCTCGTCA GTATCTGCAA CACAGTGAA
1801   AAAGTATAAT GATATTCTAA ATGCGCACAC CTCATTATGC GGGACAACAG
1851   TATTTGGGAT AGTAAACAAC CAAAGGTTTA ACTATTTAAA GTCAATCGTT
1901   AATCAAGAGC ATATATGTCT AAGAAGTTTC ATCTGTGGTA TTGCAATGAT
1951   ATGTTTAAAA CCTCTCGTTA AGGATTTTCA CCGTACAATA GTATTTACTA
2001   TTCCCATAAA TTTAAGAAAC CACTTAGGCT TAGGTGGGTC ATTGGGTCTC
2051   TTCTTCAAAG AACTAAGGGT CGAATGTCCA CTTTCTCTAA TTGATGACGA
2101   ACTTTCGCC AACGAATTTT TGACCAACAG TAACGATAAC GAGGATAATG
2151   ATGATGAGTT TAATGAAAGA TTGATGGAAT ATCAATTTAA TAAAGTTACA
2201   AAGCACGTTA GCGGTTTTAT TATGGCAAAA CTGAGGAGTT GGGAAAAGAA
2251   TGGGTTTAAT GATGACGATA TAAGGAGGAT GAAGTATGAC AATGACGACG
2301   ATTTCCATAT CCAAATTCA AGGACAAAAT TGATTCAAAT CAATGATGTT
2351   TCCGACATAT CGTTATCGAT GAACGGCGAT GACAAATCTT TCAAAATTGT
2401   AAGTACGGGA TTTACAAGTT CGATAAATCG CCCCACATTA ATGTCTCTTT
2451   CCTATACATA CTGTGAAGAG ATGGGCCCTGA ATATCTGTAT TCACTACCCT
2501   GATTCGTATA ATTTAGAATC TTTTGTAGAA TGCTTCGAAT CTTTATATGA

2551   ATAG GCAGGT GACGCATTAA ATATATGTCT GTATAGTACG TATTTTTCCT
2601   ATTTTATTTA TTCTTATCAA AATTTAATCA ACATATATGC TAAAGAAACT
2651   ATTGATAGGA GATATGACAG GAAATGACAC TGTTCCTGGA ACTTTGGCAT
2701   GCCGAGGCCG TCATTTCCAG TATAACTGAG CAAAAGAAG TGACGGTAAA
2751   TACA

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FIG. 6

YPL272C protein sequence.

MTTFRPLSSFEEKILTQSLNDQRNGTIFSSSTYSKSLSRENDADWHSDEVTLGTNS
SKDDSRITLPLIATTLKRLIKSQPALFATVNEEWEFEPLKQLKTSDIVNVIEFET
IKDKEVNCHWGVPPPPYLLRHAFNKTRFVPGSNKPLWTLYVIDEALLVFHGHDLVLF
DIFSAANFHKLFLKELNEISTVTHSEDRI LFDVNDINLSELKFPKSIYDSAKLHL
PAMTPQIFHKQTQSFFKSIYYNTLKRPFGYLTNQTSLSSSVSATQLKKYNDILNA
HTSLCGTTVFGIVNNQRFNYLKSIVNQEHI CLRSFICGIAMICLKPLVKDFSGTI
VFTIPINLRNHLGLGGSGLGLFFKELRVECPLSLIDDELSANEFLTNSNDNEDNDD
EFNERLM EYQFNKVTKHVSGFIMAKLSWEKNGFNDDDIRMKYDNDDDFHIQNS
RTKLIQINDVSDISLSMNGDDKSFKIVSTGFTSSINRPTLMSLSYTYCEEMGLNI
CIHYPDSYNLESFVECFESFIE

FIG. 7

YGR131W DNA Sequence

```

1      TGCAAAACT GATAAGGGCT TTCCTGCTGA TCGCCTTGCT GATTTTGCGT
51     ATTTGCCGAA GATTGATTGA TCAATTGCGT AAAGGGGTCG TCTTCTTGAC
101    GGTTGATATT GAATAGCATG TTTTGAATAC GTAGTTGATT GACCTCTTTC
151    TTTTAATTGC GTGCAGCTGC TCTCAGGTTT AAGATGTACG AGGGTCCACG
201    GGGTAGCAAG CACAAGAACG ATGATATATA TGACAGAACG ATGGATAAGA
251    ATGGTATGTT GTCTGCACTG TTCAGCATTC GACTACCCCT CTCCCGGTTT
301    TTTTCTCCTC GTTTC AATTT AAAAAGCAA CTCGCTACCC GGCCGCACAC
351    CCCTTATTCC TGTT CAGCCG TTTAAGGTGA GAACCCTTTA CTTCATAGCC
401    TTTGTAGATC TTTCTATTGC TACCATTGAA GGGTCGGTGA CGTGGAAAT
451    TTGACATTTA TCAGTGGCGT ATTGGGAGGC AAGCAATTGA AAGAACTGTG
501    ATTTATTTCC GCTTGTTTCA AATTATTGAT GTTTAGCACT TTGCAGTAGC
551    GACAATACAA TATATGTGCT TTTAGTGCTG GGATAGTTTC TAGCTCCATT
601    TCGGGGCGCT TGTTACATTT ATTGTATATG CGCGGATGTG GCACATGCTG
651    TTGAGATCTC ACTCCTTTGG TATCTCTTTC CTGCGCCGCA TTGTGCCGGC
701    AGAATGTCGC GCTTGTTATC TCATGAACTT TTCCTCTTTA CGAACCCTTT
751    GGCGGCATGC CGTTTAAAAT CTGTTGAAGA TTTCTTTTAC GAACAATGAG
801    CAATGTTTTG CACAGGCAGG TGGGAAGTAG GGCCTATCGC GCCTTGGAATG
851    CAGATATAAG TATAAATATA AATTATAATA ATTGGCTGTA TCAGTAAATC
901    CTTCTTGCGA TGGGAGGAAG CACGATAGAG TATGTTAAGC TTTTGAGAGG
951    CTTCATATTC ATTGGAATTT TAAATAACAA TAAAGCAACA ACAATAATAA

1001   ATGCTATCAG CTGCAGATAA TTTAGTGCGC ATCATAAATG CTGTTTTTCT
1051   TATTATATCC ATAGGTCTAA TCAGCGGCCT GATAGGTACA CAGACAAAGC
1101   ATAGTTCTCG AGTGAACTTT TGTATGTTTG CCGCCGTTTA TGGTCTGGTT
1151   ACGGATTCAT TATATGGGTT TTTGGCTAAT TTCTGGACAT CATTAAACATA
1201   CCCAGCAATT TTGCTTGTTT TGGATTTTTT AAATTTTATA TTTACGTTTG
1251   TAGCAGCCAC CGCTTTGGCT GTAGGTATAA GATGCCATTC GTGTAAAAAC
1301   AAAACATATC TGGAACAGAA TAAGATCATA CAAGGCTCAA GCTCCAGATG
1351   TCATCAATCT CAGGCTGCTG TTGCGTTTTT TTACTTTTCC TGTTTTCTAT
1401   TCCTCATCAA AGTGAAGTGT GCCACGATGG GTATGATGCA AAATGGTGGA
1451   TTTGGCTCTA ATACCGGATT CAGCAGAAGG AGGGCAAGAA GACAAATGGG
1501   CATACCTACA ATTTCCAGG TTTAA

1526   GCCTA CTGGACTGAA AAAAAGGCAA
1551   TTCGCGTACA ATTTTCGTTG ATCGTTCTTT ATATAACCTT TGCATTAAAT
1601   AAATTTAACA AAAAAAGTTC TTTCTAAAAT AATATTATGG TGATACATGA
1651   ATGTGCTTTA GTTTTTTCGT AGGCTCATCC ATGTATATAT ATAAATGATA
1701   AAAAATAAG TTACGATATT GATAG

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FIG. 8

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YGR131W Protein Sequence.

MLSAADNLVRIINAVFLIISIGLISGLIGTQTKHSSRVNFCMFAAVYGLVTDSLY
GFLANFWTSLTYPAILLVLDLNFIFTFVAATALAVGIRCHSCKNKTYLEQNKII
QGSSSRCHQSQAAVAFFYFSCFLFLIKVTVATMGMMQNGGFGSNTGFSRRRARRO
MGIPTISQV

FIG. 9

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YDR453C DNA Sequence

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1      GTAGATGAAT TCAAATCTAT GATTAAGAAC AATGAATTCA TTGAATGGGC
51     GCAATTCTCC GGTAAC TACT ATGGTAGTAC TGTCGCTTCC GTCAAACAAG
101    TCAGTAAATC TGGTAAGACT TGTATTTTAG ATATTGATAT GCAGGGTGTC
151    AAATCTGTCA AGGCTATCCC AGAGTTAAAT GCCAGGTTT TGTATTATTGC
201    TCCACCATCG GTCGAGGATT TGAAAAAAG ATTAGAAGGT AGAGGTACGG
251    AGACCGAAGA ATCCATCAAC AAGAGGTTAA GCGCCGCTCA AGCTGAATTG
301    GCATATGCTG AGACAGGTGC CCATGACAAA GTTATTGTCA ATGATGATTT
351    GGACAAGGCC TACAAGGAAT TGAAGGATTT TATCTTTGCA GAAAAATGAT
401    GTAGCCCTAT ATAGACATTA CTAAGTATGT ACCTGGTAGG AGAGTGCTGT
451    CGCAAAGCGA CAAAACGTCC AATTATTCAA TTAATATAGT GTAAAAGTTC
501    TCAACGGGCT TATGCTAGTT TTTTGTGTTA GTAAGCGCTA CGACGACTAG
551    AACCATCTCT TGAATTTCCA AGTGCCAAAA TCAATGACCA CGGATACTGT
601    GGCCAGGAAT CTGTTGGTTG GTCATCCTCA AGATCTAGAC AATATCATAT
651    TGGGCCAGTA TCTGATTATC TTAAC TATAT GCGCCCCTCT AGTTTACAAG
701    TTTTAGTCAT TGGGGGTG GAGGGCTGAT CCCCCTTAC AATTGGCGTC
751    GTTTAGGAGC GGGCGAGGCT CTCCTTTCTC TTACACACTT GCTAAGGTGT
801    TTGTTACCCG AGTAATCAAG GATCAACTAT GGATGAGATT TAGATTAACG
851    TATTTAGAGC AGACGATTGT AAGAATATAT TTTGTAATTT CGATTGTTTT
901    TTGCTACTTA CATTTGTTTAT CTTGAAATAT CCAAAGTGAA CACTATTACT
951    GTTTTTTGCT CAAGAATATA TTAGCCTTAC AAGAACGTAA AAAACCAATC

1001   ATGGTAGCAG AAGTTCAAAA ACAAGCCCCA CCATTTAAGA AAACCGCCGT
1051   AGTCGACGGT ATCTTCGAGG AAATTTCACT GGAAAAGTAT AAAGGTAAGT
1101   ACGTTGTTCT AGCTTTTGTC CCATTGGCTT TTTCATTTGT CTGTCCAAC T
1151   GAGATTGTTG CGTTTTCCGA TGCCGCCAAG AAATTCGAAG ATCAGGGCGC
1201   CCAAGTTTTA TTTGCCTCCA CCGACTCTGA ATATTCCTTA CTGGCATGGA
1251   CCAACCTTCC CAGAAAAGAC GGTGGATTAG GTCCAGTTAA AGTTCTTTG
1301   CTTGCTGATA AGAATCATTC CTTATCCAGA GACTATGGCG TTTTGATTGA
1351   AAAAGAAGGT ATAGCTTTAA GAGGTTTGTT CATAATCGAC CCGAAGGGAA
1401   TCATTAGACA TATCACTATC AATGATTTAT CTGTTGGCAG AAACGTCAAT
1451   GAAGCTTTGA GATTAGTCGA AGGTTTCCAG TGGACTGACA AAAATGGTAC
1501   AGTTTGTCCA TGCAACTGGA CCCCAGGAGC CGCCACCATC AAACCTGACG
1551   TTAAAGATTC CAAGGAGTAT TTCAAAAATG CCAATAATTA A

1592                                     TCTTCGCAC
1601   GATAACGCTA GGCCCTATTA AATAATTAAA AATACATCAC CCTATATATG
1651   ATAAGAAAGA TGGTTTTGTA TTATTATGAA ATTGACTTGA AAGAATAGTG
1701   TAACAAAAGA AAAAGAAACT GTAATTGAAG AATGATATGC ATTTCTATGT
1751   GTATATTAAC TTAATCATCT TTATATCCAG AAGACGCAA T

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FIG. 10

YDR453C Protein Sequence.

MVAEVQKQAPPFKKTAVVDGIFEEISLEKYKGKYVVLAFFVPLAFSFVCPTEIVAF
SDAAKKFEDQGAQVLFASDSEYSLAWTNLPRKDGGGLGPVKVPLLADKNHSLSR
DYGVLIEKEGIALRGLFIIDPKGIIRHITINDLSVGRNVNEALRLVEGFQWTDKN
GTVLPCNWTPGAATIKPDVKDSKEYFKNANN

FIG. 11

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WO 00/58520

Ergosterol Biosynthetic Pathway

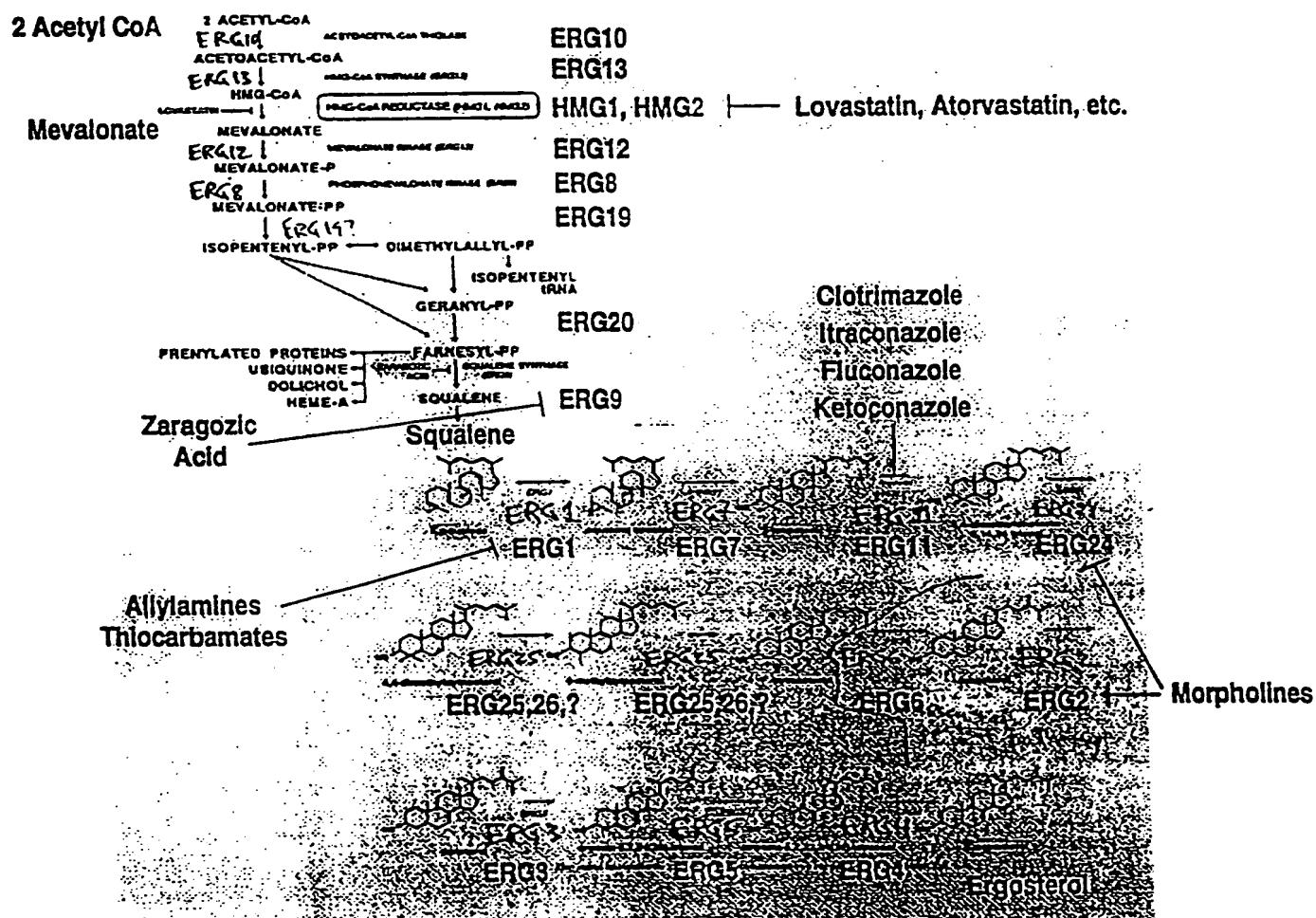


FIG. 12

Clotrimazole Titration Plot

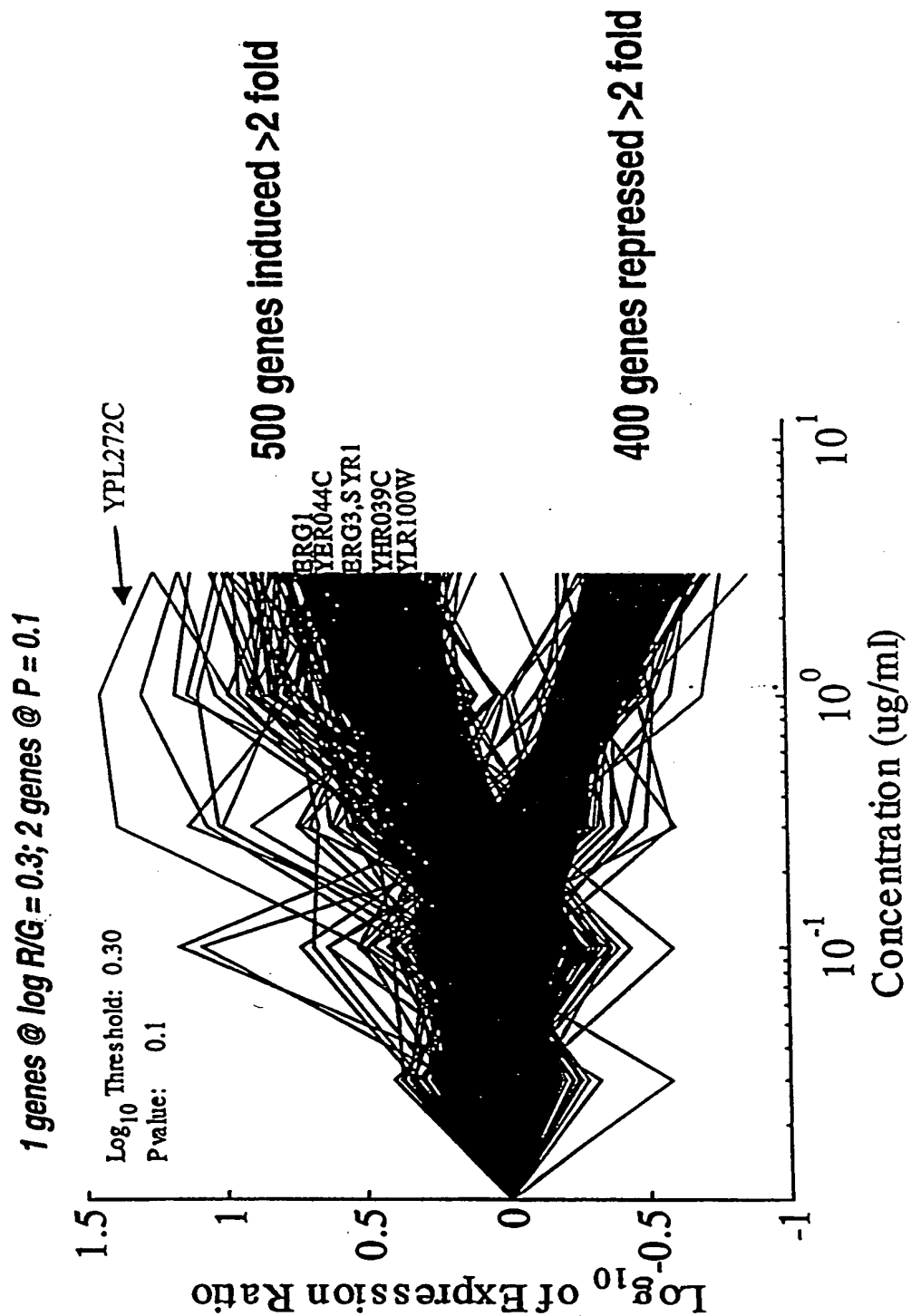
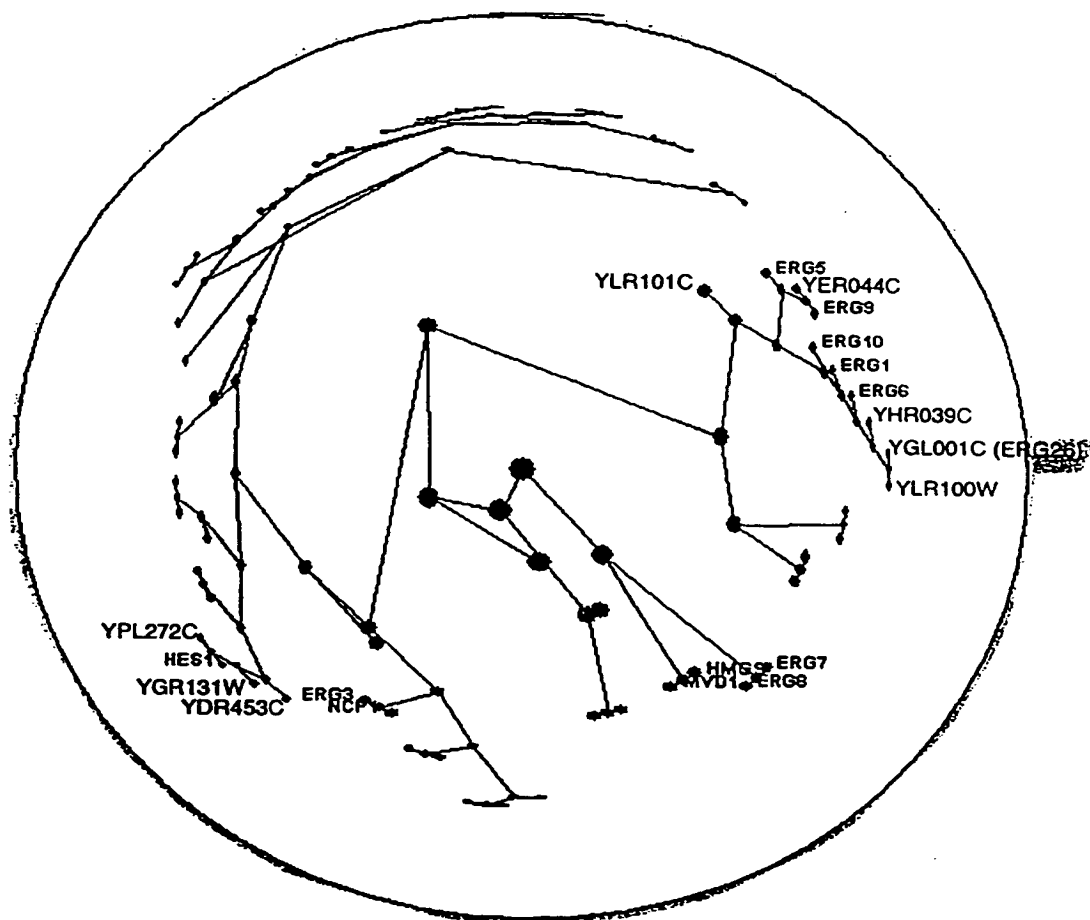


FIG. 13

**FIG. 14**

Identification of Pathway-Specific Reporters

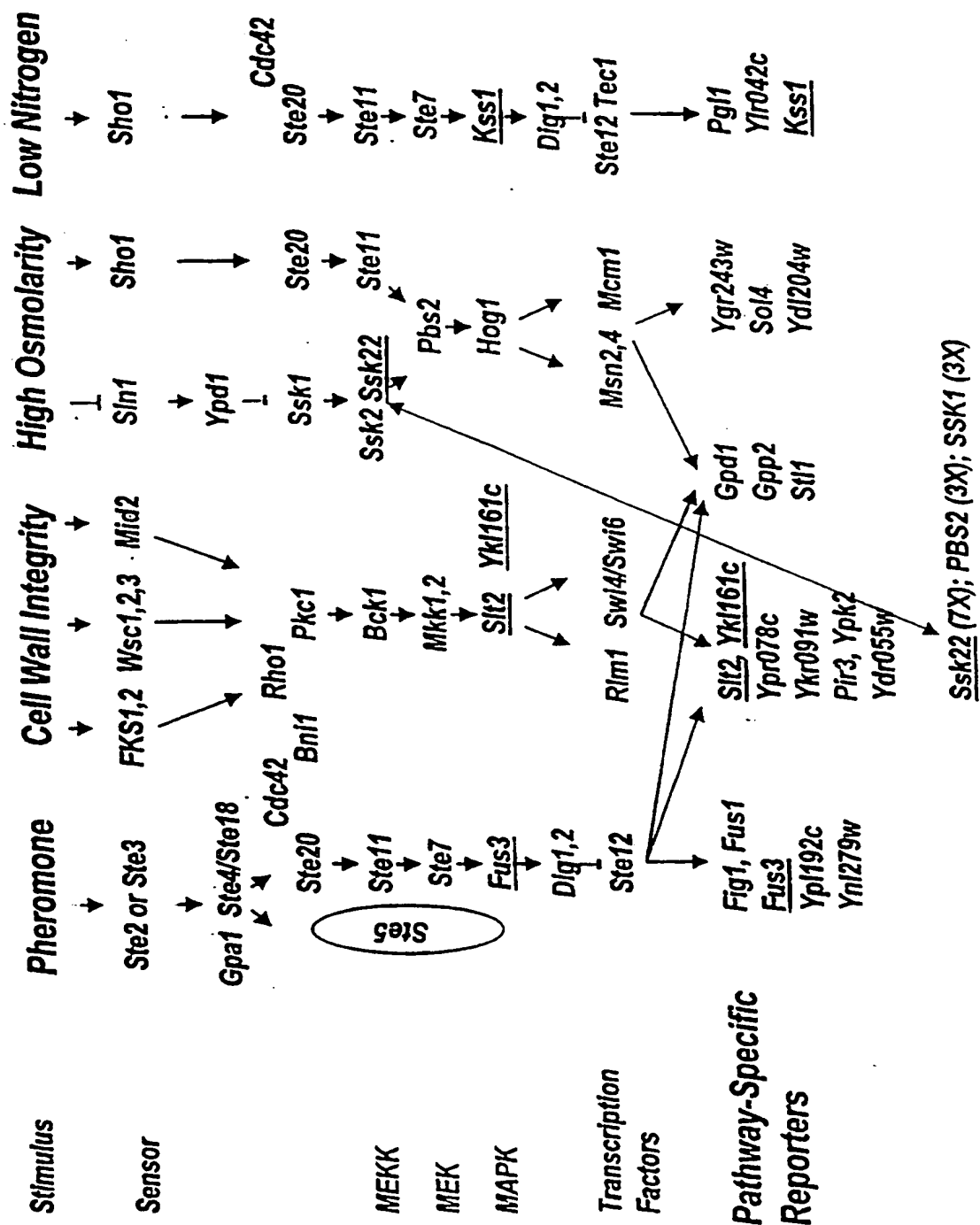


FIG. 15

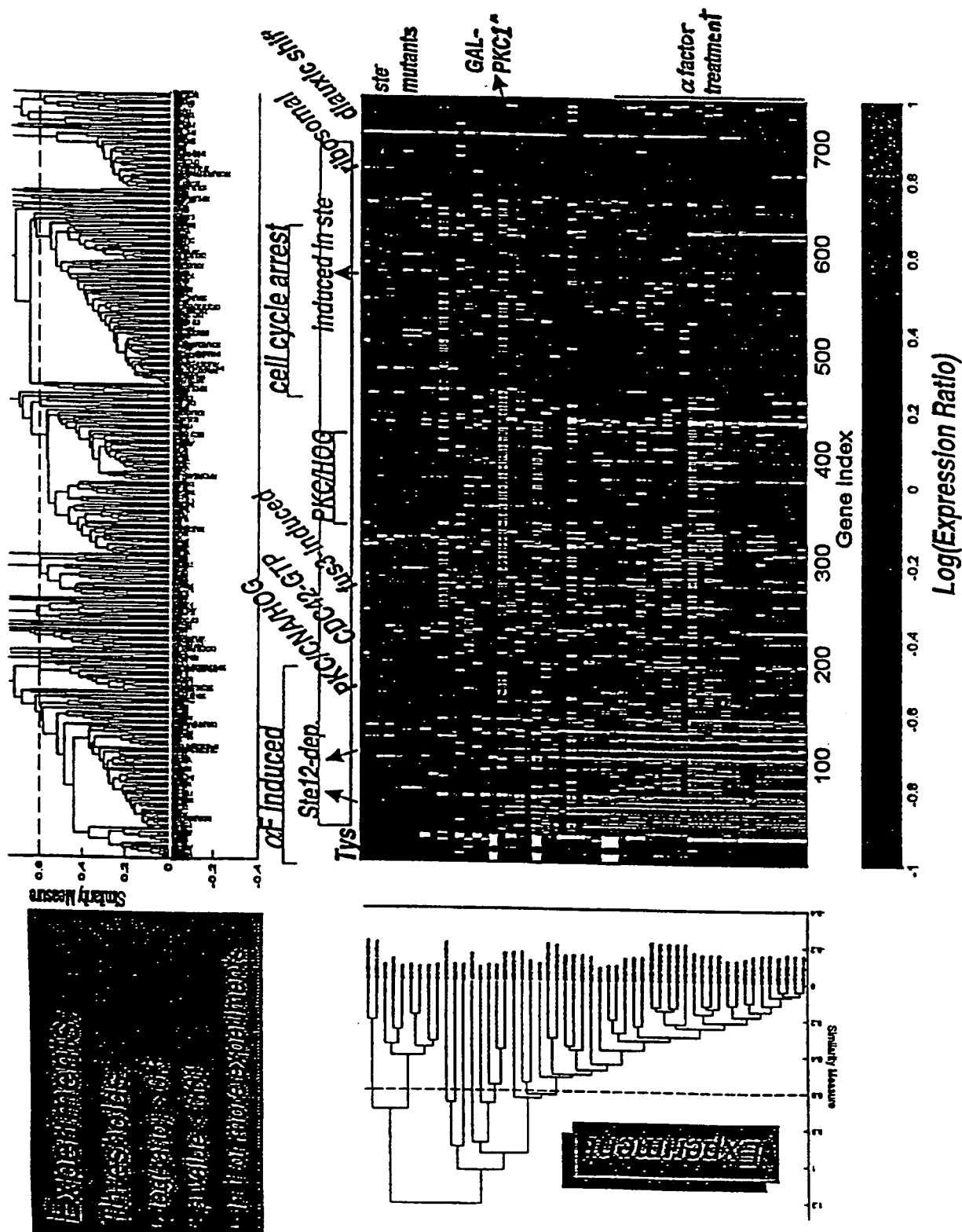


FIG. 16

SLT2 (YHR030C) DNA Sequence

(including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

GTGGTGAAAATGAAGGAAATTTACAAGATTGTGGATGACGAAGTTGTCATGGACA
TGAGATTAGTGAGTCGGGTCAATTGGTAATCCCTTGTTAAAGGAATCAAAGGAGTT
TCGTCAAGATTTGAATGCCAGGCCATTAGCTAGATTGGAACGTTTGAAAATCTTG
ATAAACTATGCAGTTAAGATCTCTCCGCATAAGGAAAAATTCCCCTATGTGAGGT
GGACAGTGGGTAAAAACAAGTACATACATGAGCTCATGGTCCCAGAGCGCTTTCC
CATTGATATTTCCCAGAGAAAATGTCGGGTTAGAAAGAACTCAGATTCCATTAATG
CTATGCTGGGCACTGTCCATTCATAAGGCACAGGGTCAAACCTATTCAAAGACTAA
AGGTGCACTTGAGGAGAATTTTCGAAGCCGGCCAAGTTTATGTTGCACTGTCAAG
AGCGGTAACTATGGACACCTTACAGGTCTTAACTTTGATCCAGGAAAGATTTCGC
ACCAATGAAAGAGTAAAAGATTTCTATAAACGTTTAGAACTTTGAAATGACTTG
CAACGAATAAATGCATATACTCTAGTTGAAGTTTTCTTTCTTGTCTATACAGG
TTCGAATACTTGTGAGCCTATCTGTATAATTTAACAGAATCCCGAAATATTCATC
TAGAAGCCATCTATTTAGCTAAGCCTACGTATGCGGCGATTTTATATTATCTTT
TTTTTTTTTTATAGAAGACTGCGAAATGTTGGCAGAATGGAAAGTTTCAGTGTTA
AAAATAGAACTGAAAAAGGAGATCTAGCCAGGAATATATCGAAAAAAAAGTGA
GGGAAATCAGATCCTACACAAATATTTAGATTTAATTGAAGACCCTGGTCTGCCA
GATATATATATATATTAGACGAACTGTGCATTCAAGTCAGTCAGCAAATCTAGGCCACAG
ATTTTCTTATTGAAGCTATCAAAATAGTAGAAATAATTGAAGGGCGTGTATAACA
ATTCTGGGAGATGGCTGATAAGATAGAGAGGCATACTTTCAAGGTCTTCAATCAA
GATTTCAAGTGTAGATAAGAGGTTTCAACTTATCAAAGAAATAGGGCATGGAGCAT
ACGGCATAGTGTGTTCAAGCGCGTTTGCAGAAGCTGCCGAAGATACCAAGTTGC
CATCAAGAAAGTGACAAACGTTTTTTTCGAAGACCTTACTATGTAAAAGATCCCTA
CGTGAGCTAAAGCTTTTGAGACATTTCAAGAGGCCACAAAATATTACATGTCTTT
ATGATATGGATATTGTTTTTTTATCCAGACGGGTCTATCAATGGACTATATCTTTA
TGAGGAACTTATGGAATGTGATATGCACCAAATCATCAAATCCGGTCAACCTTTG
ACGGATGCTCACTATCAAAGTTTACATACCAAATATTATGTGGTTTAAAGTATA
TTCATTCTGCAGATGTCTTGCATCGTGATTTGAAGCCCGGCAATTTGCTTGTCAA
TGCAGATTGTCAATTGAAAATCTGTGATTTTGGGTTAGCTAGAGGTTATTTCGGAG
AATCCTGTGCGAAAACAGTCAATTTTTGACGGAGTACGTGGCCACTAGATGGTATA
GAGCTCCGGAAATAATGTTGAGTTACCAAGGATATAACCAAGGCGATTGACGTATG
GTCAGCTGGCTGTATTTTAGCGGAGTTTCTTGGTGGAAAGCCAATCTTCAAAGGA
AAGGATTACGTTAATCAATTGAATCAAATATTACAAGTTTTAGGGACACCCCCAG
ACGAACTTTAAGAAGGATTGGTTCTAAAAATGTTTCAGGACTACATACATCAATT
AGGTTTCATTCCAAAAGTACCTTTTGTCAATTTATACCCAAATGCCAATTCACAA
GCATTAGACTTATTGGAGCAAATGCTCGCGTTTGACCCTCAAAGAGAAATTACCG
TGGATGAGGCCCTGGAGCATCCTTACTTGTCTATATGGCATGATCCAGCTGACGA

FIG. 17A

ACCTGTGTGTAGTGAAAAATTCTGAATTTAGTTTTGAATCGGTTAATGATATGGAG
GACTTAAACAAATGGTTATACAAGAAGTGCAAGATTTTCAGGCTGTTTGTGAGAC
AACCGCTATTAGAAGAGCAAAGGCAATTACAATTACAGCAGCAGCAACAGCAGCA
GCAACAGCAACAGCAACAGCAACAGCAGCCTTCAGATGTGGATAATGGCAACGCC
GCAGCGAGTGAAGAAAATTATCCAAAACAGATGGCCACGTCTAATTCTGTTGCGC
CACAACAAGAATCATTTGGTATTCCTCCCAAATTTGCCAAGGCATGATGCAGA
TTTCCACCTCGACCTCAAGAGAGTATGATGGAGATGAGACCTGCCACTGGAAAT
ACCGCAGATATTCGCCTCAGAATGATAACGGCACGCTTCTAGACCTTGAAAAG
AGCTGGAGTTTGGATTAGATAGAAAATATTTTTAGGACAAAAAACTATAAGTAAC
CGGGGAAGTATAGAATCACCATAGATGTAAGCTTACAGACAATGTGTATATATGA
TGTATATGAACGTATACAAATATATATATATATACGTGCTCTTGTTGTAGCTCGT
ATATCAAATTCCTCCTCCGACGCTTATCTTAATCGTACTCCGCGGAAGTTTGTTA
TCGCCTCTTGAATTCCTTCTTTTCGTTCAATTTATGATTAGTCATCTATAGACAAT
ATTCATTATTTAAGCACCTAGAATACTAACTAAATGTCTAAATATGACACAAGG
AAGATAAGATAAAAAAAACCAAGCGCTTAGAATATGACTTTAATGGTACCTTTCA
AACAAGTTGATGTATTCACTGAGAAGCCCTTTATGGGAAATCCAGTAGCAGTAAT
AACTTCTTGGAATTTGATGAAAATGAAGTCAGTCAAGAAGAATTGCAGGCAATT
GCCAACTGGACAACTTATCAGAAACAACGTTTTTTATTTAAACCATCTGATAAAA
AGTATGATTACAAGTTGAGGATCTTTACTCCAAGAAGTGAATTGCCATTTGCTGG
TCACCCAACCATTTGGTTCATGTAAGGCTTTCCTTGAGTTCACCAAAAACACCACT
GCGACTTCTCTCGTCCAGGAATGTAAAATAGGCGCTGTTCCAATAACAATTAATG
AGGGACTAATTAGCTTCAAAGCTCCGATGGCTGATTACGAAAGTATATCGAGTGA
GATGATTGCTGATTATGAAAAAGCGATTGGTTTGAAATTCATAAAGCCTCCTGCT
CTTTTACATACTGGGCCAGAGTGGATCGTGGCGCTAGTAGAAGATGCAGAACTT
GCTTCAATGCAAACCCAAATTTTGCTATGCTTGCACACCAGACAAAACAGAATGA
CCATGTGGGAATTATCCTAGCGGGCCCTAAAAGGAAGCCGCCATCAAAAACCTCC
TACGAAATGAGGGCGTTTGCTCCGGTGATAAACGTTTATGAAGAT

FIG. 17B

SLT2 (YHR030C) Protein Sequence.

MADKIERHTFKVFNQDFSVDKRFQLIKEIGHGAYGIVCSARFAEAAEDTTVAIKK
VTNVFSKTLCKRSLRELKLLRHFRGHKNITCLYDMDIVFYDPDGSINGLYLYEEL
MECDMHQIIKSGQPLTDAHYQSFTYQILCGLKYIHSADVLHRDLKPGNLLVNADC
QLKICDFGLARGYSENPVENSQFLTEYVATRWRAPPEIMLSYQGYTKAIDVWSAG
CILAEFLGGKPIFKGKDYVNQLNQIILQVLGTPPETLRRIGSKNVQDYIHQLGFI
PKVPFVNLYPNANSQALDLLEQMLAFDPQKRITVDEALEHPYLSIWHDPADPEPVC
SEKFEFSFESVNDMEDLKQMVIQEVQDFRLFVRQPLLEEQRQLQLQQQQQQQQQQQ
QQQQQQPSDVDNGNAAASEENYPKQMATSNNSVAPQQESFGIHSQNLPRHDADFPP
RPQESMMEMRPATGNTADIPPQNDNGTLLDLEKELEFGLDRKYF

FIG. 18

YKL161C DNA Sequence

(including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

AGTAATACTTGC AAATATTG CAAAACCTTGGAAGAATGTTAATGAATCATTTCTTG
CACCATTCTTTCAATCATCTCAATCTCCTGCTGTGATGTTTAAGTATAACATTGA
AGACTATGCCCTAATTTCCAATGTTATTTAGTTTTTAAGCATATCTTTGTTTCTAA
CAGGAAACTCAGGCCACATCCGCAAAAAAATATGTGCCAAAAAACTTTCAACAC
TTCAAAGATACTTACCACTGCAGGAAAATAATCTACGTGTAACGGTTTGAAAATA
AATTTGACTTCATAATTGGACATAAGTACTCCATCGCCATCCCTTTTTTAAAGAAG
TTTCCACAAGAATGAATGGCTAATCGCAACTAAATCTTTTCCTTGCAAACGTAAC
ACAGTATCGACATTTTCTTACTCAATCCAACGAAGGAATAACCTATCTAAAAAAT
AAACGCCGTAGTTTTTCAGCCCACAAGACGTCATTAAAAGATTTGTTAATTATAAA
AATAGAAATATTTCTACCAGCATGATTATTCGTTACTTGAAAGTCCCCAATAAAT
TTCACTGTTTTCCGTTAACTGTTGTAGTTATTAAACGCAGCAAACAGATTATTTTG
AACAAACACCGGAGAAACACGCGCAGACCCATTTCGAGTTAAAAATAGTAACTCGCG
ATCAATCAATGCAGGAAGCACCGTAGGAATTAGTAAGAACTCGTATTTTGATTGA
AAATGCCATGAAAGCAATTGACTTGCTGCAGTAAAAAGCGCTGCCACAACTTTG
TAATTTTCGACAATGACGTTCTTTTCAGATGGTTACTGTCTTTTTTTTGAAGAAA
CAAAAGAAGGTACTTTTATGATGTTATACTAGGCCAAAAAGCCTATTTAATGTAAG
TCCTAATTGTCGTTTGAGACTGGATGAAAAGGGACAAAATGGAAGGATAACTAAA
GGTGACTTACCGCCAGATTAATTCGGCCTGGAATAGTTTGATATCGAAGAAAGAT
TCACAATTAAATGGCGACTGACACCGAGAGGTGTATTTTCCGTGCATTCGGCCAA
GATTTTATCCTAAATAAACATTTTCATTTGACAGGTAAGATTGGTCGGGGCTCAC
ACAGCCTTATTTGTTCTTCAACTTACACAGAATCGAACGAGGAACTCACGTGGC
TATCAGAAAAATACCAAACGCGTTTGGCAATAAACTATCTTGCAAGAGAACTCTT
CGTGAATTGAAACTACTAAGACATTTAAGAGGGCACCCAAATATAGTGTGGCTCT
TCGATACTGATATAGTATTTTACCCAAATGGGGCACTAAATGGCGTTTATTTATA
TGAAGAACTAATGGAATGTGACCTTTCTCAAATTATAAGGTCCGAACAACGCCTG
GAAGACGCACACTTTCAAAGCTTCATATATCAGATACTGTGTGCTCTGAAATACA
TACATTCTGCTAATGTTTTACATTGTGACCTGAAACCAAAAAAATCTTACTTGTTAA
TAGTGATTGCCAACTAAAAATTTGTAATTTTGGGCTATCGTGTAGTTATTCAGAA
AACCACAAGGTTAACGACGGCTTCATTAAGGGTTATATAACCTCGATATGGTATA
AAGCACCAGAAATTTTGCTGAATTATCAAGAATGCACAAAAGCTGTCGATATTTG
GTCAACAGGCTGTATCTTGGCCGAACCTTGGTAGGAAACCAATGTTTGAAGGG
AAGGATTATGTAGATCATTTGAATCATATTCTACAAATACTTGAACACCACCTG
AGGAAACATTTGCAGGAAATTGCCTCTCAAAGGTGTATAATTATATCTTTCAGTT
CGGTAATATCCCGGGAAGATCGTTTGAAAGCATACTACCTGGTGCTAATCCAGAA

FIG. 19A

GCGCTTGAATTGCTAAAGAAAATGCTAGAATTTGATCCTAAAAAAGGATTACTG
TAGAGGATGCACTAGAGCATCCATATTTGTCAATGTGGCATGATATAGATGAGGA
ATTCTCATGTCAAAGACCTTTAGATTCGAATTCGAGCATATCGAAAGTATGGCG
GAATTAGGAAACGAAGTTATAAAGGAAGTATTTGATTTTCAGGAAAGTTGTTAGAA
AACATCCTATTAGCGGTGATTCCCCATCATCATCACTATCTTTAGAGGATGCCAT
TCCTCAAGAAGTTGTACAGGTCCATCCTTCTAGGAAAGTTTTACCCAGTTATAGT
CCTGAATTTTCCTATGTAAGCCAACTTCCATCACTAACTACAACCCAGCCATATC
AAAACCTTATGGGAATAAGCTCTAATTCATTTTCAGGGTGTAACTAAAAGGAAAA
CACCTTCAAACAAGATACTAAGCATGAAAATAGTGAACACTGAACGGACCTACT
GAGCCAAATATAACAAAAATGAGCCCAGTTTTCATCGTCTCCCCAGGTCACGATA
TAAATGTCAATGATGGTACAAACCAAATAACAAATGAGGATGACAGCGATTTTTTT
CTTCGACCTAGAAAAAGAACTTGAATTATTTAGACGATAAATTTTTGTAGCAGAA
AACCACAATAATAGATGCGCACATACACTATCTATAATGAATATGTAAAATGCC
TGTTACCTTCTTAATTATTGGTATATACTTCAAATATTGCAAAAAGAGAAAGTC
CTCTCGGCGGTTTTGTCAGTTCCTTCCGAAAGCGGGAAAAACCAAATGTGAGAAA
GTAGGATACACCATTGCGTAGATTCGCGATGATCCGAATATAAACATGATTCCCT
CGTCAGTCCTCTCTCAAGTTTTCTTTCCCGTTTTTAAATAGCTTACTAATATTTTC
ACAAAAAAGTTGATATCATTTAAAGGTGCTTTTGGCGGGATTGAATGATGAAAAG
ATTACACCCCTTGAGAATTCAAGTTCATCTGAAATCTGATTACCCACTGTTTACT
TTCGAGCAATTACTCTCTACAAATGGGATAAGAAGAGGCCAAACTGCGAGAATTT
CTTTGAAAGATTACATAGAGTGGCAAAATTTCCCAAACATAATGAAAAGAGAAAA
TTTTTTTACGCAAAGGAAGCCTGTAACACTACAACCGCAAAGAAGAACCCTTTTCA
TTTGATAACATTCTTGACTGTGAGCCACAATTTAGCAAATGCCTTGCCAAATGGC
TACTGGTTAATTACAAATTAATGACTATCCTTATTACGATCTTAACATTGTGAA
TATTTACACGGATTTACCCCAAGCAATTCAGATTTGCAAAAATTTAATGTCATAT
CTCAAGTCTACTTTATCTGATAACATGTTCCAGAAAATAAATATTTTCATGGTAC
CT

FIG. 19B

YKL161C Protein Sequence.

MATDTERCIFRAFGQDFILNKHFLTGKIGRGSHSLICSSSTYTESNEETHVAIRK
IPNAFGNKLSCKRTLRELKLLRHLRGHPNIVWLFDTDIVFYPNGALNGVYLYEEL
MECDLSQIIRSEQRLEDAHFQSFIYQILCALKYIHSANVLHCDLKPKNLLVNSDC
QLKICNFGLSYSENHNVNDGFIKGYITSIWYKAPEILLNYQECTKAVDIWSG
CILAELLGRKPMFEGKDYVDHLNHILQILGTPPEETLQEIASQKVYNYIFQFGNI
PGRSFESILPGANPEALELLKKMLEFDPKKRITVEDALEHPYLSMWHIDEEFSC
QKTRFRFEFEHIESMAELGNEVIKEVDFRQVVRKHPISGDSPSSSLSEDAIPQE
VVQVHPSRKVLPSYSPEFSYVSQPLSLTTTQPYQNLMGISSNSFQGVN

FIG. 20

PIR3 (YKL163W) DNA Sequence

(including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

TCTGGCTTCGAGGAATTATTACCTAAATAGGAAAGGCAGAATATATTAGAAAAAA
AAGAAAAACCAAATGAGAAAAGTGCTGGTGCTAAATAAAACATTATTGAGGGGCC
AAGAGGGGACAAAAGAAGATATAACTAGATCATTAAGTTTTCGCTCTAGTAACAG
GAACAAAGATTGTGAGATACACTGTTATGCTAAGAGACGGTGCGATATTCTGTAC
GAAAATTATTTAACTATTTAACTAAATGTATACCACTTCACGTGCCACCGAGTAGG
TTTCTAAAATGTGCAACCATTTTAGGTATGTGCGCAGCTCTTTATTCTAAACGGG
AGTCACTACATTACTATTATCGTGTTTTTGCCCATGTACTTTCTTATAATCTTAA
GACAACAACGGGATGATAGGCGCATTTCGGACTTTCATTGATGCAAATGTGTGAAA
AATGCATCCAAAAGACAACCTTTTGTACAGAATACAATTGCAAAAATACTTTACGG
GCATAGATCGGTAAGGTCACCGGGAAGCTAGCGTAAGAGACCTTATTCGGAACCG
AGCAACCATTTCGGAATGTAGTAGTAGTTGAAGGAGTAAATCGACCTTATTGTAC
ACTACTTCCTTTAAATTTGATTTCTGGCCCCGCGCAATTTCTTGCGGTTAAGCT
GTATTTTTTACCTCATCGGGAAAAGTTATTGCAAGTTAAAGGGGATCAAACGATTA
GCAAATAATTATAGATCAAAGGCCGAGGGCTTTCTAAATTTGGCATATTTTCGCC
GTCGACTGAAATAGAAGGGATAAATCATGCATCTCCAGGATTATCCCTACTCCAT
TCATTACAACATGCGCCAAATCAAGCCTATATAAGATTCTCGTCATTTAGCATGC
TCTATTGATTTGTGTCTTGTTTTGTCTAACACTGAACTGTAACCTAAGATTTCT
TTAGATAATTATTACATTTACATCAATAAGAAATCTCATAAAACAAGTACTGTTT
ATAAGTAAAAATGCAATATAAAAAGCCATTAGTCGTCTCCGCTTTAGCTGCTACA
TCTTTAGCTGCCTATGCTCCAAAGGACCCGTGGTCCACTTTAACTCCATCAGCTA
CTTACAAGGGTGGTATAACAGATTACTCTTCGAGTTTCGGTATTGCTATTGAAGC
CGTGGCTACCAAGTGCTTCCTCCGTGCGCTCATCTAAAGCAAAGAGAGCCGCTCT
CAGATAGGTGATGGTCAAGTACAGGCTGCCACTACTACTGCTGCTGTTTCTAAGA
AATCCACCGCTGCTGCTGTTTCTCAAATAACTGACGGTCAAGTTCAAGCTGCTAA
GTCTACTGCCGCTGCTGTTTCCCAAATAACTGACGGTCAAGTTCAAGCTGCTAAG
TCTACTGCCGCTGCCGTTTCTCAAATAACTGACGGTCAAGTTCAAGCTGCTAAGT
CTACTGCCGCTGCCGTTTCTCAAATAACTGATGGTCAAGTTCAAGCTGCCAAGTC
TACTGCTGCCGCTGCCTCTCAGATTTCTGACGGCCAAGTTCAAGGCCACTACCTCT
ACTAAGGCTGCTGCATCCCAAATTACAGATGGGCAGATACAAGCATCTAAACTA
CCAGTGGCGCTAGTCAAGTAAGTGATGGCCAAGTCCAGGCTACTGCTGAAGTGAA
AGACGCTAACGATCCAGTCGATGTTGTTTCTGTAAATAACAATAGTACCTTGTCA
ATGAGTTTAAAGCAAGGGTATCTTAACCGATAGGAAGGGTAGAATTGGCTCTATCG
TTGCCAACAGACAGTTCCAATTCGATGGTCCTCCACCACAAGCTGGTGCTATCTA
TGCTGCTGGTTGGTCCATCACCCAGAAAGGTAACCTTAGCTCTTGGTGACCAGGAT
ACTTTTTACCAATGTTTGTCTGGTGACTTCTATAACTTGTATGATAAGCACATTG
GTTCTCAGTGCCATGAAGTTTATTTGCAAGCTATAGATTTAATTGACTGTTGAAC

FIG. 21A

GATGCATCGATCAATCGGAGTCGTCCTCCTTTAACTTCACGAATTAGTTGCCACT
CTCATTCCCCACACATAAACTTGTTTTATGGCATCCTTTTCATTTAGCATGTCTT
TATTTCCAAACCTTTCTCTCGTTCTTTGCATTCAATTTAGCGTTTGCTCGAGAAAGC
ATCACGTTTTTCAACATTATCGTTTCGTCGCTATAATAAAAATAGTTATAGAATTT
ACTCAGATTTACATGTCGTACCTTTTTTAATTGTAAAAAATAATTTTATGATAC
ATAATTACCTAAATATAATTCAGAATCAAACATACTTATAGCTATTTGTATGCTA
TTAGGTGGTCCTGCTATAAAAAATATCGTTTATAATACTTTATATTTTATCTTTCA
ACTTAGTCGCAATTGCAGAAGCTTTCCTGAGAAAAAATTTGTGAAGCTAGCTGC
GATAGCAAAGGAGCGCTTAAGGTATAGAAAAGCACTCAGCTGGAATGCCAAAAGA
TAGTTTAGCAACTGACCAAGGAAAAAGCTTGTAGGTAGACTTAACCTTCATTGTTC
TCTAATCCTTTCGTTCGTGTATATTGTAAAACTGCTGAACGAGTATTGATAAAAG
ATATCTTGCCACTAAGGGGCAGATCCCCTTCTGGTGTGATAGACAACCCAGGA
GCATAGATAACACCAACTTGTGGTGGAGGGTCATCGAATTGGAATTGTCTGTTGG
CAACAGTAGAACAGATGCTGCCCTTGCTATCTGTCAAAATGCCGCTCTTCAAAGT
TACTTTCAAAGCGCTGTCACTGCTACGACAGCTTTTTTTTTTAGAAACAGCAGCAA
TGCCTTGACATGTAACGTAAGAAAAGAAAAAGAGATGGCAGAAGAAATACTAAG
CGATAACGGCAATGTAGAGGTGCTTTTTTTTATCGGAATAAATAGAGAAGTCAGTA
ACAGTGATTGCTGTGGCTCCCTCTTTAATCGTATCTATGTAGGTTCCGATTAAAG
TGGTCGTG

FIG. 21B

PIR3 (YKL163W) Protein Sequence.

MQYKKPLVVSALAATSLAAYAPKDPWSTLTPSATYKGGITDYSSSFGLAIEAVAT
SASSVASSKAKRAASQIGDGQVQAATTTAAVSKKSTAAAVSQITDGQVQAAKSTA
AAVSQITDGQVQAAKSTAAAVSQITDGQVQAAKSTAAAVSQITDGQVQAAKSTAA
AASQISDGQVQATTSTKAAASQITDGQIQASKTTSGASQVSDGQVQATAEVKDAN
DPVDVVSCNNNSTLSMSLSKGILTDRKGRIGSIVANRQFQFDGPPPQAGAIYAAG
WSITPEGNLALGDQDTFYQCLSGDFYNLYDKHIGSQCHEVYLQAIDLIDC

FIG. 22

YPK2 (YMR104C) DNA Sequence

(including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

CCAACCACGTAAGGGAAAAGGACGGTGTGTTGGGCCATTATGGCGTGGTTGAACAT
CTTGGCCATTTACAACAAGCATCATCCGGAGAACGAAGCTTCTATTAAGACGATA
CAGAATGAATTCTGGGCAAAGTACGGCCGTA CTTCTTCACTCGTTATGATTTTG
AAAAAGTTGAAACAGAAAAAGCTAACAAGATTGTCGATCAATTGAGAGCATATGT
TACCAAATCGGGTGTGTTAATTCCGCCTTCCCAGCCGATGAGTCTCTTAAGGTC
ACCGATTGTGGTGATTTTTTCATACACAGATTTGGACGGTTCGTCTTGACCATC
AAGGTTTATATGTCAAGCTTTCCAATGGTGCAAGATTCGTTCTAAGATTGTCAGG
TACAGGTTCTTCAGGTGCTACCATTAGATTGTACATTGAAAAATACTGCGATGAT
AAATCACAATACCAAAGACAGCTGAAGAATACTTGAAGCCAATTATTAACTCGG
TCATCAAGTTCCTTGAACCTTTAAACAAGTTTTAGGAACTGAAGAACCAACGGTTTCG
TACTTAAACGAATGATTTACTAATGGCTTAATGATTTTCACCTTTTTCAATGAA
TATTAACGGTAAAGAAGAAAATTTCAATTTTTTGAACACATACTTTATACTTA
ATAGATCCATATTTTCGACATATTAGCAAACGATTGCATAGGTTTCTGAGTCTTTT
TTTTTTTTTTTTTTCATAAGGAGGAGAATATTTTGGTTAATCGCAGTATCTTCTTCA
TAAGTGCTGTTTCTAATTATATCTAATTCACGAATTTTTCCCAAATTAGCGTATC
CCCGAATTCAGATTACCTACCCCGAGTTTTTTTATTATATTTCCCTCGAGAAATCT
GTAAATGGCCGTCATCCTTAGATTTATAAATAAAATGATAAAATTCAGCCAAAG
TGCTCCTAAACCAGAATTGTTCAACTGGGTCAAATTATCGCGTATACAAATATAC
ATATAGTAACATGCATTCTTGGCGAATATCCAAGTTTAAGTTAGGAAGGTCCAAA
GAAGATGATGGGAGTAGTGAAGATGAAAATGAAAATCGTGGGGTAATGGCCTGT
TTCATTTCCACCATGGAGAAAAACATCACGATGGTAGCCCGAAGAATCATAATCA
TGAACACGAACACCATATAAGAAAGATCAATACAAATGAGACTCTCCCAAGTTCC
TTAAGTTCTCCAAAATTACGTAATGATGCATCCTTCAAGAATCCATCGGGGATAG
GAAATGACAATTCTAAGGCTTCCGAAAGGAAAGCTAGTCAGTCGTCTACTGAGAC
GCAGGGACCGAGTTCGGAATCCGGACTAATGACAGTGAAGGTGTATTCTGGTAAA
GATTTTACTCTTCCCTTCCCTATCACCTCTAACTCTACTATTTTACAAAACTAC
TAAGTTCCGGCATCCTTACTTCATCATCCAATGACGCTTCCGAAGTTGCAGCCAT
AATGCGGCAGCTACCACGATACAAGAGAGTGGATCAAGATTCAGCAGGGGAAGGC
TTGATAGATAGAGCTTTTGCCACTAAATTCATTCCCTCTATATTGTTACCTG
GGTCAACAAATTCAAGCCCATTACTTTATTTTACAATTGAATTTGATAATTCTAT
TACTACTATTAGTCCAGATATGGGAACGATGGAGCAACCAGTGTTTAAACAAAATA
TCGACATTTGATGTAACAAGAAAATTACGATTTTTTAAAAATCGATGTCTTTGCAA
GGATTCCATCCCTACTTTTACCCTCTAAAACTGGCAACAGGAGATTGGCGAGCA
GGACGAAGTACTGAAGGAGATTTTAAAAAAAATCAATACAAATCAGGATATCCAT
TTGGACTCCTTCCATTACCTTTGAATTTAAAAATCGATTCTGCAGCCCAAATAA
GACTATACAATCACCATTGGATTTCTTTAGAAAGGGGATATGGTAAATTAAATAT

FIG. 23A

CACGGTGGACTACAAACCTTCTAAGAACAAGCCTCTCTCCATTGATGACTTTGAT
CTATTGAAGGTTATCGGGAAGGGTTCGTTTCGGCAAAGTGATGCAAGTAAGGAAAA
AAGATACCCAAAAGATTTACGCTTTGAAGGCTCTGAGAAAAGCATATATTGTATC
GAAATGTGAAGTGACACATACTTTAGCGGAGAGGACTGTCTAGCAAGAGTTGAC
TGCCCCCTTTATTGTTCCGTTGAAGTTCTCATTCCAATCTCCGGAGAAGTTGTACC
TAGTATTAGCTTTTCATTAATGGCGGTGAACTGTTCTACCATTTACAACACGAGGG
ACGATTCAGTCTAGCACGCTCCCGTTTTTATATTGCAGAACTATTATGTGCTCTC
GATTCATTACACAACTTGACGTCATTTATCGTGACCTAAAGCCTGAAAACATTC
TATTGGATTACCAAGGACATATTGCACTGTGTGATTTTGGGCTTTGCAAGCTGAA
CATGAAGGATAATGACAAAACAGACACTTTCTGTGGTACTCCCGAATATTTGGCA
CCAGAAATCTTGTTGGGGCAGGGCTATACTAAACAGTTGACTGGTGGACATTAG
GTATCTTACTGTATGAGATGATGACAGGGCTGCCACCATACTATGATGAGAACGT
TCCTGTTATGTACAAGAAAATTCCTGCAGCAACCGCTACTATTTCTGATGGATTT
GACCCTGCGGCAAAGACCTATTAATTGGCCTCTTAAGCAGAGACCCAAGCAGAA
GACTCGGCGTTAACGGTACAGATGAAATTCGTAACCATCCTTTCTTTAAAGACAT
CTCATGGAAAAAGCTACTTTTGAAGGGCTATATTCCGCCTTACAAGCCAATTGTA
AAGAGTGAAATAGATACTGCAAATTTTGATCAAGAGTTCACTAAGGAAAAACCGA
TCGATAGTGTAGTGGACGAGTACTTAAGTGCAAGTATTCAAAAGCAGTTTGGTGG
GTGGACGTACATTGGTGACGAACAGTTGGGTGATTCTCCTTCGCAGGGGAGAAGC
ATTAGTTAGAAGCAAGCCGAAGCAAGCCGAGCCGAGCCGGACGGAATTTATAGCT
ATAGCCGCAAGAGGTTGCAATTTTCAAAAATGGATAGTTCAAGTAGATTGCGATA
CGCACTCCGTTACTATTGTGGTTAACGGGGACAAGAAGAACTACAGAAAATAGAA
TGGTCCGCAGAGGCTGCGCTCTTCTTTTAGCAACTCTCACACGACTTATGTTGCT
TATTCATTTCTTTTACAGCATTATCAGAATTCCTCCATCTACGGAATTGAGATCA
AAGACCGACCTGTTGTCGGCCGAAGGACGGACGCTTATACCCGCGGATGTCAAAG
CGAAGCCCGCGGGGCGCAAGTCGAGGTTACCGGAATTCGCCAAACGGCAAAGGAC
CCTTGCAATTGCCTGAAAGGAAAGATTGCTTTTCTGTTTGTTGCCACTTTTCTTA
CATAGTCTGGGCGGGAGCAGCTTATTTCTTCCGCGGATGATCCTGGATTTCTT
GCGCGGGCTCAGCCATGGGGAGCCTTACCTAGTCCCGTAAAGGGAAAAAGCTAAC
CTCATTCGCCTCACAGGGTGAAAGCGTGAACAAAAAAGAAAAGCTTAATGA
TTAAAATTTACAGTATATATATATTTGTATTTACGTATTAACTATATATAAATA
GATATGTATGCCGAAAAAGTAAAGTCTGGGTGATGCCTAGTCCAATCTTCTTAC
TACTGTCCAGTTTCTATCGTAGCAGTTAATTATACATAGAACTGTGTAAATTCAA
CGCATTAATTTTTTTTTTTTCACTTTCGCAGTTAGGGGGGACACATTTTTTTTG
CCCTTTCTTAAGCTTCGTAAGCGAGTTACATCATTATTTCTTCTGCGGATACAAT
ACGCGTTCGTACAAGTCACAGCTGGACCGTATAGGGAACAAGACTGCAACTCTCT
CCAACCTTGTTAAACAGAGGAGGAAAAGAAAGAGGGAAAAGAGGAACAAAGACAAT
CAAAGAAAAAGAATAGAAA

FIG. 23B

YPK2 (YMR104C) Protein Sequence.

MHSWRISKFKLGRSKEDDGSSSEDENEKSWGNGLFHFHHGEKHHHDGSPKNHNHEHE
HHIRKINTNETLPSSLSSPKLRNDASFKNPSGIGNDNSKASERKASQSSTETQGP
SSEGLMTVKVYSGKDFTLPFPITSNSTILQKLLSSGILTSSSNDASEVAAIMRQ
LPRYKRVDQDSAGEGLIDRAFATKFI PSSILLPGSTNSSPLLYFTIEFDNSITTI
SPDMGTMEQPVFNKISTFDVTRKLRFLKIDVFARI PSLLLPSKNWQQEIGEDEV
LKEILKKINTNQDIHLDSFHLPLNLKIDSAAQIRLYNHHWISLERGYGKLNITVD
YKPSKNKPLSIDD FDLKLVIGKGSFGKVMQVRKKDTQKIYALKALRKAYIVSKCE
VTHTLAERTVLARVDCPFIVPLKFSFQSPEKLYLVLA FINGGELFYHLQHEGRFS
LARSRFYIAELLCALDSLHKLDVIYRDLKPENILLDYQGHIALCDFGLCKLNMKD
NDKTDTFCGTPEYLAPEILLGQGYTKTVDWWTLGILLYEMMTGLPPYDENVPVM
YKKILQQPLLFPDGFDPAAKDLLIGLLSRDPSRRLGVNGTDEIRNHPFFKDISWK
KLLLKGYIPPYKPIVKSEIDTANFDQEFTKEKPIDSVVDEYLSASIQKQFGGWTY
IGDEQLGDSPSQGRSIS

FIG. 24

YLR194C DNA Sequence.

(including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

GGATATGATTGCTGAGAATGCGTTACCGGCCAAAACAAAGACAGCGGGATTGAGA
AAATTAAAGAAGGAAGATATTGACCAAGTTTTTTGAGTTGTTCAAAAGATATCAAT
CCAGGTTTCGAACTAATTCAAATTTTCACAAAAGAAGAATTCGAACATAATTTTCAT
TGGTGAAGAATCGTTACCATTTGGATAAACAAGTAATTTTCTCATATGTAGTCGAA
CAGCCCGATGGAAAAATTACAGACTTCTTCTCATTTTACTCATTGCCATTCACAA
TCCTAAATAACACAAAATATAAGGACCTAGGCATCGGGTACTTGTATTATTATGC
CACCGATGCAGATTTCCAATTCAAAGACAGGTTTGATCCAAAAGCTACTAAGGCT
TTGAAAACAAGATTGTGTGAATTGATTTATGACGCTTGTATTTTGGCCAAAACG
CTAATATGGATGTTTTTAACGCGTTGACTTCGCAAGATAATACATTGTTCTTGGA
TGATTTGAAGTTCGGGCCCGGTGACGGGTTCTTGAACCTTCTATTTATTTAATTAT
AGAGCAAAGCCGATTACCGGTGGCTTGAATCCCGACAATAGTAACGACATTAAAA
GGCGTAGCAATGTCGGTGTGTTATGTTGTAGTGGCTGAAAGGACGAGGCGTATA
TAGTTTTCGTGTACATAGCCGACAGAATTTGACCACATTTAGTTTTTCCGCATAG
TCAATTGACGAAGTGAAAAAATAATTAATCCAATGGCTGGCTTTAGAGTGTCAGC
CTCCAAAATAAATCCAAAATAGACAAAGAGAATCACTATAATTACCGCCTTGGA
GTCCAAGTTGGCTTGAGAACTCGCATTTATTTTTAGCGACTGAGGTAGCTGAAAA
ACGCCTACTTTCTCAGAAGGCGGTAGTGAGCATATATAAGTATGTAAGAAAGATC
AACTCTTCTGGACTAGATACTCACCGATCTAGTGAAAATATAAAACAAACCCAACA
TATATATAAAATGAAGGCCTGTTCCATATTATTTACCACCTTAATTACTCTAGCC
GCTGCTCAAAAAGACTCTGGTTCCTTAGATGGCCAGAACTCTGAAGATAGCTCAC
AAAAGGAAAGCTCAAACCTCTCAAGAGATCACACCTACCACGACAAAGGAAGCCCA
AGAAAGCGCATCAACTGTAGTTTCTACCGGAAAAAGCTTAGTACAACTAGCAAC
GTCGTCAGCAACACCTATGCTGTGGCTCCAAGTACCACCGTAGTGACGACGGATG
CACAAGGCAAAACACGACACAGTACCTATGGTGGGTGGCCGAAAGCAACTCTGC
CGTAAGCACAACTTCAACTGCCTCTGTGCAGCCACCGGAGAGACGTCAAGCGGA
ATCACCAACTCCGCATCCTCCTCAACGACATCAACATCAACGGACGGGCCAGTTA
CTATAGTAACTACCACGAATTCGTTAGGTGAGACTTACACATCTACTGTTTGGTG
GCTACCGTCCTCAGCCACAACCTGACAACACGGCTTCATCAAGTAAATCATCTTCG
GGATCCTCATCAAAACCGGAATCAAGCACCAAGGTAGTAAGCACTATCAAATCAA
CTTATACCACTACGTCAGGTTCTACAGTAGAGACACTGACCACTACATACAAGTC
TACAGTCAACGGTAAGGTAGCGTCCGTAATGTCCAATTCTACCAATGGCGCCTTT
GCCGGCACTCACATAGCTTATGGTGCGGGTGCAATTCGCCGTTGGTGCCCTTTTGT
TATAGAATGTATAATCAGTTCTGTATACCACCACATAGTTCTGCATTTTAAATAAA
ACTCTTTCTTTTTTATACACTGTAGGTAACCAATAATACTATTGTTATCATCG
TGCTTGCGTATTTTTTTTTCTTTTCGGGTGAAAACTCCGCAGTATTTCTCGCTCTC
CCTGGATAATAAGCTAGAAAAAAAATATATATGACAGATGGATGAGTAATCAT

FIG. 25A

ATTCAATAAGTATTGTCTGGCTTCTGAGACGGCGGTAAGATATCCTTAAGAGTTG
CAATGGTCCTTTTACACAAAAGCACACATATATTTCTACCGATTTTGCCTCTGT
TTCACGCGCCTTTTTTAATAGATACCCCAATCCATACTCCCCCATGTACTATCC
ATAGACACAATATCAAGGAACGTTGATCAAGAAGGAAATTTGCGCACAACGAGGC
TGTTGAAAAAGTCCGGAAAGCTGCCACATGGGTCAAACCCTTTTTAAGAGGTAT
AACAGAAACATGGATAATCGAAGTTTCCGTAGTGAACCCCGCTAACTCCACAATG
AAAAC TTACACTAGGAATCTGGATCACACTGGAATCATGAAGGTTGAAGAATATA
CTACCTATCAATTTGACAGTGCTACAAGTAGTACGATAGCAGACAGCCGGGTGAA
GTTTTCAAGTGGCTTCAATATGGGTATCAAATCTAAGGTAGAGGATTGGTCGCGC
ACTAAATTTGACGAAAACGTTAAGAAAAGCAGAATGGGCATGGCATTGTGTTATCC
AAAAACTCGAAGAGGCGAGAAATCCTCAGTTTTGATGTTCCCATTTAAAGATCTT
TAAAGATATCACCATGGGCGAGCGAAATTGAGAAAAC TAGTGCAGCTCGCATTTG
GTCACGTCCTAAAAATTGTAAATAAGCGCTGGTTCAACAAAATTTAATATACACA
CATATATAATTATTTATTTATAACAGTCATTCTGCTAAACTATACATCAAATGTC
ACTAATCTTGATATT

FIG. 25B

YLR194C Protein Sequence.

MKACSI LFTTLITLAAAQKDSGSLDGQNSEDS SQKESSNSQEITPTTTKEAQESA
STVVSTGKSLVQTSNVVSNTYAVAPSTTVVTTDAQGKTTTQYLWWVAESNSAVST
TSTASVQPTGETSSGITNSASSSTTSTSTDGPVTIVTTTNSLGETYTTSTVWWLPS
SATTDNTASSSKSSSGSSSKPESSTKVVSTIKSTYTTTSGSTVETLTTYKSTVN
GKVASVMSNSTNGAFAGTHIAYGAGAFV GALL

FIG. 26

PST1 (YDR055W) DNA Sequence

(including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

TCTTGTTCTTTACAGATTCAAGAGGAAACCAAAAAAATCAAAGAAAAGAATC
GAATTTTTTCCCAAATGAAAGTGTAAGGAAAAAAGAGGAGATAGAAAATCCG
AAGAACCCCAAGGGACGGACAAACACAAGACGATGCTGCACGTGGTTAGTTTTGT
AAGCGCAGGTTACGATAAAGAGCATAAACAAATCATTACTAAGAGCGGTATACAA
GAATAAAGTGACAAACAGTTCTCCCTATTTAACGCACTTAACGTAGGTTCCATCA
TTATGATGCTATTGCCACATCAAATCTCCTTTGGACTGAACCCGCATTAGTAATT
GCCCCTTTTTCTTTTCTTCCGCGGGTGGGCCCCATAAATAGAAAAAAAAGAAAG
AAAGCGTTTAAATAAATAGAGTGAGCGGATTTCTATTATCTGAAAACCGGGTTAT
AATGCACGTGATATGCACGTGGGAGCTGGGCGGCTATTTTTTTCTTTTTCAAATG
TATTTGAGTCGTTTAAATAGCACTCCCCGTTGACCCGCCAACTCATTTTTGTTT
TCTCTTTACGGAAAAGGCTTTAAATTAAGGCCCGCATTTTCGGTATCCTTGAGGG
AAAAAAACCAAAGAAACCCAAAAAAGACCACAAAGCTGGGATATCTTAATTAGTA
GAGAGGGCTTTTAGTTTTAATAGTGTTACGAGTCTCTAAAAATAGCGTAGGCACA
CTGCCCTGATTTCGGACTTTGATCAGAGTTTATTACTACAAAGAGTAATGTTGAAT
GATTGGGCTGGGTTTTTCATAGCATTAACCTCTAAGTAATATCATTC AACCGCTCAA
GGTTCCTTACGAGCAAACCCATATATGCTCTACAGATAAACATATAAATAGCGTG
CATATTCTTCTCTATTCAACTCTTGCTCTGTATAGTTCAATAGAATCTTACAGTA
CATCACGCTGCAATAGATCTAATCCAAGAGAGAAGCAAAAAAAGCTCGCTA
TAAAAATATCATGCAATTACATTCACCTTATCGCTTCAACTGCGCTCTTAATAACG
TCAGCTTTGGCTGCTACTTCCTCTTCTTCCAGCATACCCTCTTCCTGTACCATAA
GCTCACATGCCACGGCCACAGCTCAGAGTGACTTAGATAAATATAGCCGCTGTGA
TACGTTAGTCGGGAACCTTAACCTATTGGTGGTGGTTTGAAGACTGGTGCTTTGGCT
AATGTTAAAGAAATCAACGGGTCTCTAACTATATTTAACGCTACAAATCTAACCT
CATTCGCTGCTGATTCTTGGAGTCCATCACAGATTCTTTGAACCTACAGAGTTT
GACAATCTTGACTTCTGCTTCATTTGGGTCTTTACAGAGCGTTGATAGTATAAAA
CTGATTACTCTACCCGCCATCTCCAGTTTTACTTCAAATATCAAATCTGCTAACA
ACATTTATATTTCCGACACTTCGTTACAATCTGTGATGGATTCTCAGCCTTGAA
AAAAGTTAACGTGTTCAACGTCAATAACAATAAGAAATTAACCTCGATCAAATCT
CCAGTTGAAACAGTCAGCGATTCTTTACAATTTTCGTTCAACGGTAACCAGACTA
AAATCACCTTCGATGACTTGGTTTGGGCAAACAATATCAGTTTGACCGATGTCCA
CTCTGTTTCTTTCGCTAACTTGCAAAAGATTAACTCTTCATTGGGTTTCATCAAC
AACTCCATCTCAAGTTTGAATTTCACTAAGCTAAACACCATTTGGCCAAACCTTCA
GTATCGTTTCCAATGACTACTTGAAGAACTTGTGCTTCTCTAATTTGTCAACCAT
AGGTGGTGCTCTTGTGCTTGTAAACAACACTGGTTTACAAAAAATTGGTGGTCTC
GACAACCTAACAACCATTTGGCGGTACTTTGGAAGTTGTTGGTAACTTCACCTCCT

FIG. 27A

TGAACCTAGACTCTTTGAAGTCTGTCAAGGGTGGCGCAGATGTCGAATCAAAGTC
AAGCAATTTCTCCTGTAATGCTTTGAAAGCTTTGCAAAAGAAAGGGGGTATCAAG
GGTGAATCTTTTGTCTGCAAAAATGGTGCATCATCCACATCTGTTAAACTATCGT
CCACTTCCAAATCTCAATCAAGCCAACTACTGCCAAGGTTTCCAAGTCATCTTC
TAAGGCCGAGGAAAAGAAGTTCACCTTCTGGCGATATCAAGGCTGCTGCTTCTGCC
TCTAGTGTCTTAGTCTGGCGCTTCCAGCTCTAGCTCTAAGAGTTCCAAAGGCA
ATGCCGCTATCATGGCACCAATTGGCCAAACAACCCCTTTGGTCCGTCTTTTGAC
GGCAATCATCATGTCTATAATGTAATGGAATGAAGAAATATTCTTCATTTTTGAT
AACTAGTACCTGTCATTACGACATGTGAACAAATAAAAACATTTATTTAAAAAT
TTTATGTATTCAAATATTTTCGGGAAAGAGATAAAAGTAACGACACTTAAAAAT
TAAAAAATCACAATACTTTATTTACTCAGTCTTTTGATCAGCTCCGGCACCTCCT
TGTTGTTGCTTCTTTGCTGAGCCCGCAACAAAATTGTAAATCAATAGGCCTAAAA
GTAACATTTTCCAGTTCCTTTGAAACCAAGACACCTCCTTAACCTCTTCATCTTC
TTCGAATTGTGCAGTGCTTCCATCCTTATTCTTACTAGCTTTTTTTATCAGCATAA
GTTTTGGTTTTCTTCTTTAATTTGGTGACTGGTGCAGTAGGTCCCGCTTCTGGAT
ATCTGACTGTAGCAGTAATAGCATCGTTAGTCTCGTCATATGATAACGACACTTG
TTTGACCTCATTATCTTCATCTACATCCACAATTAAATCGTATTTTAGTGGTGTC
CTCAGCTTCATGTAGCTAAAACATGGCATATCCAGCTTACCTTCAATCTGGGCAT
TCAAACAGTATTCTCCAGAACTTCAACATCCTGTATATTAACGGTTGTTACTGT
AACATTCCCATCGGATGTACTATCAATCTCAAATGTTCCCTAGGGGTATAGCGTCT
TTCGCATCATCTGAATAGCTTAATTGTAAAATATCAGCACAGAAAACCATGCTGG
CCAATAAAATCACACGCAACAGCCGCACAAGCATCTTTCCTTCAATGAGTATTGT
ACAGTTCTTGTTAGATAGTGTTGAATAGTACCACCTTGTTTTTTTACTCAAAGTG
TCTTTTATATACTTCTAATTATTCTATATTTGGTTGGGTTTTTTAAGTTACCAAT
GCAAATACAGTGGTTAGAGACCCAGCGCACGTATGCAAAAAAATACAGCGGAAAT
TTCAAGTAAAAATGTAGCTTCATAAAAAAGAAGCA

FIG. 27B

PST1 (YDR055W) Protein Sequence.

MQLHSLIASTALLITSALAATSSSSSIIPSSCTISSHATATAQSDLDKYSRCDTLV
GNLTIGGGLKTGALANVKEINGSLTIFNATNLTSFAADSLESITDSLNLQSLTIL
TSASFGSLQSVDSIKLITLPAISSFTSNIKSANNIYISDTSLQSVDGFSALKKVN
VFNVNNNKKLTSIKSPVETVSDSLQFSFNGNQTKITFDDLWANNISLTDVHSVS
FANLQKINSSLGFINNSISSLNFTKLNTIGQTFIVSNDYLNLSFSNLSTIGGA
LVVANNTGLQKIGGLDNLTIGGTLEVVGNFNTSLNLDLKS VKGGADVESKSSNF
SCNALKALQKKGGIKGESFVCKNGASSTSVKLSSTSKSQSSQTTAKVSKSSSKAE
EKKFTSGDIKAAASASSVSSSGASSSSSKSSKGNAAIMAPIGQTTPLVGLLTAI I
MSIM

FIG. 28

KSS1 (YGR040W) DNA Sequence (including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

TTGGGATTCCATTTTTTATAAGGCGATAATATTAGGTATGTAGATATACTAGAAGTTCTC
CTCGAGGATTTAGGAATCCATAAAAGGGAATCTGCAATCTACACAATTCTATAAATATT
ATTATCATCATTTTTATATGTTAATATTCATTGATCCTATTACATTATCAATCCTTGCGTT
TCAGCTTCCACTAATTTAGATGACTATTTTTTCATCATTTGCGTCATCTTCTAACACCGTA
TATGATAATATACTAGTAACGTAAATACTAGTTAGTAGATGATAGTTGATTTTTATTCCA
ACAGTATTTATGTTTTGTCATTCCTTTCTACATAATCTTGAAACTAGGTAGATCTACAAT
TGAAAAGTAAATACTAACATTTATTACTAAATTTAAGTTAGAAATCGGCACGAAAAAAT
TTGACAGATTACGAGAGTCCAGCCAAAATATGAGTATATTACTATTTCCCTTGGTGAAA
GAAATGAAAGATGTTATTTTTTACCGGCTTAGTAATACTGAGCTACTTACTTGGGGGAAA
GAAAGATTGGCTACTTATTATGTATGAAGCCTCAGATTACCTTGAATTCCTCAACCGTTT
GAGCAGTATGCTCTTCAAATTCGAACTTTTTGAACATCTTTCCTCCACATTCTTGATTTT
TTCACATTCAAACGCGCTGTGAAGCTGTTAGAAATTTACAGATCGAGGCATATTTCTAT
ATATAATGTATTTTTTATTAAGACACCCAAAGTACTTCCAATCTGTAGATATTGCACTTTA
TCTGACCAGAAGCCAGACTTGAACAGTTACATATTGTGCTTTGCAGTCGTTAAATTTCCC
GAAGTGTTCGATTTTTTTTCTTTTCTTCTTCCACTGGATCAGATCAAAGCCGA
CTAAAAATTTGGCAATTTAAAGAAAGCATCTTTAAAGATAGAAAAGGTTATTTCAACAA
AAAAGTATCTTTTCTACTTTTCTTTCAACAATTCAAAGATGGCTAGAACCATAACTTT
TGATATCCCTTCCCAATATAAACTCGTAGATTTAATAGGTGAGGGAGCGTACGGAACAGT
ATGTTTCAGCAATTCATAAGCCTTCCGGCATAAAGGTAGCTATCAAGAAAATACAACCGTT
TAGCAAAAAATGTTTGTACAGAAGTATACGTGAGATCAAGCTTTTACGGTATTTCCA
TGAACACGAAAACATAATAAGTATATTGGATAAAGTAAGGCCAGTATCCATAGACAACT
AAACGCTGTTTATTTAGTCGAAGAGTTGATGGAACCGATTTACAAAAAGTAATTAATAA
TCAGAATAGCGGGTTTTCCACTTTAAGTGATGACCATGTTCAATACTTTACATACCAAAT
CCTCAGAGCCTTAAAGTCTATTACAGTGCACAAGTTATCCATAGAGACATAAAGCCATC
AAACCTGTTACTAAATTCCAATTGTGATCTCAAAGTCTGCGATTTTGGACTAGCGAGGTG
TTTAGCTAGCAGTAGCGATTCAAGAGAAACATTGGTAGGATTCATGACGGAGTACGTCGC
AACGCGATGGTACAGGGCACCCGAGATAATGCTAACTTTTCAAGAGTACACAACCTGCGAT
GGATATATGGTCATGCGGATGCATTTTGGCTGAAATGGTCTCCGGGAAGCCTTTGTCTCC
AGGCAGAGACTATCATCATCAATTATGGCTAATTCTAGAAGTCTTGGGAAGTCCATCTTT
CGAAGACTTTAATCAGATCAAATCCAAGAGGGCTAAAGAGTATATAGCAAACCTTACCTAT
GAGGCCACCTTGCCATGGGAGACCGTCTGGTCAAAGACCGATCTGAATCCAGATATGAT
AGATTTACTAGACAAAATGCTTCAATTCAATCCTGACAAAAGAATAAGCGCAGCAGAAGC
TTTAAGACACCCCTTACCTGGCAATGTACCATGACCCAAGTGATGAGCCGGAATATCCTCC
ACTTAATTTGGATGATGAATTTTGGAACTGGATAACAAGATAATGCGTCCGGAAGAGGA
GGAAGAAGTGCCCATAGAAATGCTCAAAGACATGCTTTACGATGAACATAATGAAGACCAT
GGAATAGTATTCACAAGAACATTTCTGCCATACTTCTAAAATTTCCCTATATTTCAGCTTA
GCAGTGACACGTTGTGGTCTGTAGGTCAATGTGAAGTAAGAACTTCAACTCACATATG
CACGATGCATGCCAATGGAAAAATGCAAGGAACGAAATGGCGCCACGGCAACAAGTTTTT
TTTTTTTCGCCAGCAGAAGTACACGAAATGCGGCTTCATGAGCCTCTTCACTGCTTTGCCT
AAACGGGAAATGCAGAGAAAAACCAGCCATCGCGTGTGCTTGGAGAGCTGACGCGACTGT
AATCAAAGAGGCGATATCAACACCTTTTATCCAGCACTATTCAACAGTGAATGGGCTCCC
AAGTAAGTCTTGGCATTGTGCTTTCTATTCTTAAGTATTAAGTAGAAGTTTTGTTTACTG
GGTTTGTATTATCCTGGCTAGATGTTTCGCATTTCGTTTTCTAGTTGACCATATTTACCAA
TATTCACAACATAATCCAGCCAAGGTAGTCTAAAAGCTAATTTCTCTAAAAGGGAGAAA
GTTGGTGATTTTTTATCTCGCATTATTATATATATGCAAGAATAGTTAAGGTATAGTTATAA
AGTTTTATCTTAATTGCCACATACGTACATTGACACGTAGAAGGACTCCATTATTTTTTT
CATTCTAGCATACTATTATTCCTTGTAACGTCCCAGAGTATTCCATTTAATTGTCCTCCA
TTTCTTAACGGTGACGAAGGATCACCATAACAACACTACTAAAGATTATAGTACACTCTC
ACCTTGCAACTATTTATCTGACATTTGCCTTACTTTTATCTCCAGCTTCCCCTCGATTTT
ATTTTTCAATTTGATTTCTAAAGCTTTTTTGCTTAGGCATACCAAACCATCCACTCATTTA
ACACCTTATTTTTTTTTTTCGAAGACAGCATCCAACCTTTATACGTTCACTACCTTTTTTTT
TACAACAATTTCAATCTTCATCCTATGAAATGACGAAAATAACCAGA

FIG. 29

KSS1 (YGR040W) Protein Sequence:

MARTITFDIPSQYKLVDLIGEGAYGTVCSAIHKPSGIKVAIKKIOPFSKKLFVTRTIREI
KLLRYFHEHENIISILDKVRPVSIDKLNAVYLVEELMETDLQKVINNQNSGFSTLSDDHV
QYFTYQILRALKSIHSAQVIHRDIKPSNLLLNSNCDLKVCDFGLARCLASSSDSRETIVG
FMTEYVATRWRAPPEIMLTFOEYTTAMDIWSCGCILAEMVSGKPLFPGRDYHHQLWLILE
VLGTPSFEDFNQIKSKRAKEYIANLPMRPPLPWETVWSKTDLNPDMLDLKMLQFNPK
RISAAEALRHPYLAMYHDPSPDEPEYPLNLDDFEWKLDNKIMRPEEEEEVPIEMLKDMLY
DELMKTME

FIG. 30

PGU1 (YJR153W) DNA Sequence (including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

AATACTGAATAGAATCACGCTACTACGACAAGACTCGGTTACTGTGCCTAAAATAATCCT
GTGATAAACGAGTTATGTTAAACGCGAGTACAGGGGTAAAGGGCATTGAGTTTTTGTGAG
TGGAAATGCCCCGTTATAGCTTCCAGTTTAATTACAAATTATCAATTTAAGCAAATATA
ACTGGAGGATTGGGGAGGCGACTAAAAATGGCTACCACGCTATTAGACATACAACATTGA
GTATTTTATGTAATTTTGTACTGCTAGCACGGCCATGCAATTGGCAACTGAAAGCTATC
TGACAACTTAAATGATTCTTAAACAATGACGACTATAATCTTCTCTAAGAAGTTTCATA
TCCATCTTCCTCATTATTACAGTTTCTTTTCTCTTGAAAGTATCGTAAAGAACAACGTC
TTCACATTAGCTATTAGAAGACCATTGAACCTACCGGATATGAGTAAGAGTGATCTTGCCG
GAGAGATAATAGCTGCACAAAGGCCAAGGATTAGATTAATGGGTGCATTGTACGAAAAAA
AATAGTTTACAGTCATTTATTCGCAATAAATCAATTTTTTTTTTCAAAAAATATGTAAGTC
TGATAAAAAATTCTTCACTGAAGAGAGATGCTTACATTCTAATTCTTGAATAAAAGACTC
TCTAACGCTGTGAATTCTCTTTAGCTGTAAACGGAAACAGAGAGTTATTCCGTAGTCACTG
AATTTTTTTTTTTTGACGCTATTATTTAAACCTAGGATATCCGTCCCATACAAAACGGC
CACGAGTTTCAATCCCAGAATGTACGAGTTATAATTCTCCTAGATGCATGATACTCGTGC
ATTCGTTTAAACAATCATACCAATTTCCCATTTTCGGGATATTAACATGAACATACTTTT
TTACTGTGAGAATGTGGTTTTCACAATTATTCATACAGGTATAAAAAACGCACAGAACTTC
AAACGGGAAGACTATCTACCCACATTGATGGACAAACGCAATGATTCTTGCTAATTCATT
ACTTATTTCCACTTTGTGCGCTTTTGCGATCGCAACACCTTTGTCAAAAAGAGATTCCCTG
TACCCTAACAGGATCTTCTTTGTCTTCACTCTCAACCGTGAAAAAATGTAGCAGCATCGT
TATTAAGACTTAACTGTCCCAGCTGGACAGACTTTAGATTAACTGGGTAAAGCAGTGG
TACTACTGTTACGTTTGAAGGCACAACCACATTTCAGTACAAGGAATGGAGCGGCCCTTT
AATTTCAATCTCAGGGTCTAAATCAGCGTTGTTGGTGCTTCGGGACATACCATTGATGG
TCAAGGAGCAAAATGGTGGGATGGCTTAGGTGATAGCGGTAAAGTCAAACCGAAGTTTGT
AAAGTTGGCGTTGACGGGAACATCTAAGGTCAACCGGATTGAATATTAATAATGCTCCACA
CCAAGTCTTCAGCATCAATAAATGTTTCAAGTTTAAACCATCAGCGACATAACAATTGATAT
CAGAGACGGTGATTCGGCTGGTGGTCATAATACGGATGGGTGTTGATGTTGGTAGTTCTAG
TAACGTTCTAATTCAAGGATGTACTGTTTATAATCAGGATGACTGTATTGCTGTGAATTC
CGGTTCATTAATTAAGGATTTATGAACAACCTACTGCTACAATGGCCATGGTATTTCTGAGG
TTCTGTTGGTGCCGTTCTGATAATACAGTCAATGGTTTCTGGGCTGAAAAATAACCATGT
TATCAACTCTGACAACGGGTTGAGAATAAAAAACCGTAGAAGGTGCGACAGGCACAGTCAC
TAATGTCAACTTTATCAGTAATAAAATTAGCGGCATAAAAAAGTTATGGTATTGTTATCGA
AGGCGATTATTTGAATAGTAAGACTACTGGAACCTGCTACAGGTGGCGTTCCCATTTTCGAA
TTTAGTAATGAAGGATATCACCGGGAGCGTGAACCTCCACAGCGAAGAGGGTTAAAATTTT
GGTGAAAAACGCTACTAACTGGCAATGGTCTGGGGTGTCAATTACCGGTGGTCTTTCCTA
TTCTGGATGTTCTGGAATCCCATCTGGATCTGGTGCAAGCTGTTAATCCTCTTTTAAAGT
ACTCATATGACTATACATACCTTCTTTTCTTTTCTTACTATTCAATACATAACAGAACA
AAGATGCAGGAAAAATATTGGTATTTGTTTCGGCAATTTATGCTGGGTTTTTTTGTAATTC
AGGTCTAATTATTACTGTTGATTTGTATCAAGTTGGTATCTTTTTTGCCATTTAATAATA
GAGATACGCTATGCTCATCCGATAGCAACAATGAGAGCCTAAAAGTCCTAATTGAGAAG
AAAACTCTGTTCAAGACTATAGTTTATGTTTCAATCTGGACCCTTGGGATCGTCTGAAA
CAGGAAGGTCAATAATTGGTAAAAAAATGGTAAATGCGACTAAGTACTACAATTGAAAC
GAATGAGCGCACTTCATCTTCCTACAAAACGCTGCGGCTGAAAAAGTTACATAAAAAACC
GTCCTCAATAGCGTTAATCCAGCGTACATGAGAAAGTAATGACAAAGTCTTCGGTAATAT
CAGTGCATCTACCAATATGACACAATTGTGAAACTTCGCTGACTCAAATAATAGCCCTGT
TTTTTTGACCATTGTTACCCATCGAGCCAGTGAGAAAAAAGCCAAAATATCTTTAAGGCC
TTCTCCATTTTATGTTTATCGATATTGTGTTGCTGCAATATTGAAATTTTAAAGGCTAT
TTACTTTGCGCTCTTGTATATAAATAAGTCTGCCGAATTATGCAATATATAGCAAAAGCTG
AAAATAGATGTAATTACATAATTTCGCAGTTGTATATGAGTATCCTTAACTCGTACATTCC
AGTTCATCTGTGACAAGGCACTGTTTTCCCTAATAATTATTAGGGAAACGTCCTTCAAAA
ATCAAAATAATTTTAGAGAGTCTCATCAACCTTCGCCATAGTTCGTGATGAAACTTTAC
GGTACGTCAGACTTTAGATATTGATTTTTTTATTATTTCTCCCATCGTGAGTACAATTAC
CCTAGTTCGAACCTATATCTTTCATTA

FIG. 31

PGU1 (YJR153W) Protein Sequence:

MISANSLLISTLCAFAIATPLSKRDSCTLTGSSSLSSLSTVKKCSSIVIKDLTVPAGQTL
LTGLSSGTTVTFEGETTTTFQYKEWSGPLISISGSKISVVGASGHTIDGQAKWWDGLGDSG
KVKPKFVKLALTGTSTKVTGLNIKNAPHQVFSINKCSDLTISDITIDIRDGDSAGGHNTDG
FDVGSSSNVLIQGCTVYNQDDCIAVNSGSTIKFMNNYCYNGHGISVGSVGGSDNTVNGF
WAENNHVINSNGLRIKTVEGATGTVTNVNFISNKISGIKSYGIVIEGDYLNKTTGTAT
GGVPISNLVMKDITGSVNSTAKRVKILVKNATNWQWSGVSTITGGSSYSGCSGIPSGSGAS
C

FIG. 32

YLR042C DNA Sequence (including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

TTCTCGAGCATTAGATGATTAAATCAAATGACATAGTATTTTCGCAACCTTTTCAGTTGGG
CTTTGTTTAAAGAAGTGAATACTTTTGCTTGAGTTGTTTAGTTTATTTTATCCACTGTT
GTCTTAACAAATATTTTCAAGACCGGTAAGCCGAAGATGAAAAATCATTATTAACCTCATT
TTTTGAACAAAAATATAAACAAAAGAAAGGCAACGCACAATTTTAGAGATACATAAAACG
CAGTGGATGTTAAAAATAACAGCGGTACAGAAACGCCTGTCTCGCTCCAATAATAATTAT
ACAAATTTGAAACCGAACGCAATGTGCCAAGAAATGTAAACACACTATAGAAAAAATAG
AACGGTGCACATTGTGCTAGCATATCTGCTTGGTTCTGAACAAGAAGCACCTGGCCACTT
TCTCCTAGCCCAATTCTTGCCAAGTTTTCAACCTCAATCTTTTGTGTTTGAACAAGCATG
TATGAGGGGTCAAATTTAGTGGAGGCCGCTTACAATCCTTCTATTTCTCTGGACCTCA
TTAGCCGTCTGGCCAGACCTAAGCGTCATAATCTGGAGAATTTTCATTGCATGCGAGAATA
TGATAAGTAAAGAACTTGTATTTATTAACAAGTTCCACCCACTCATACACGGCTACAATTA
TGACGTATAATAACGTTTCGTCTAGCCCACTTTTACTTTTGACGTTTTATTCTTTC
GAGGATTTGGCCAAGAATGCCCCGAACAGCGGAAAAAATGGCGTCGCAGTTTCAGATGTA
TAGACTCATCTTGTAGAAAAAGAATGCAAGAATGAAGTCTTTTCGTGGTGTTTTGAAAA
CACTATAAACAAACCGTCAACAAACATTTTGTATAAATATTTAGCTATATATTGAATATC
TTGACCAGTAAAGCACCTTGAGAAATTGTAAGCTTGAAGAACGTACTTTGATATCCCTCC
GTTTCATCATCTTATAGCTCGTCAACAAATCAAAAAAATATGAAGATCAGTCAATTTGG
CTCTTTAGCTTTTCGCCCCAATTGTGCTACTACAACCTGTTTCATTGTTCAAGCGCAACTTCT
CACAGATTCAAATGCTCAGGATTTGAATACTGCCCTTGGACAGAAAGTGCAATACACCTT
TCTTGACACTGGAAATTTAACGATCAACTACTTCATCTTCCAAGCACCACTCTTCCAG
CATTATTACTGGTTTCATTAGCTGCTGCTAATTTTACCGGTTCTTCATCATCGTCGTCTAT
ACCAAAAGTCACTTCCAGCGTCATAACATCTATAAATTACCAATCCTCAAATTTCTACGGT
AGTCACCCAGTTCACGCCATTGCCTTCTTCGTGCGAGAAATGAAACAAAAAGCTCTCAAAC
AACTAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTCAGTCAAGCCATGTCT
TFACTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACAAATATATTAGG
TTCAAGGTCTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCTTAAGTATGATAAAT
AAAAAAAACCTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTTTTAGTTTAAAT
ATTTCAAACGTTATCTTTCATTGAACGCCCAAATAGGGAAAAATCCTGGCAAATTTTTAT
TGCTGTCATCCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTAAAAAGACACTC
TCAATCGAGAAAGTTTATCTTTGTTATTCTGCTTTACCTGATCATATTCCGGCGTATTG
TTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTACAACATTCTTGAAAATAT
TGCGTATCAATGATATTTGCTCCTTCTTTCTCCCTCATTAAAAATATTCTCCTGGTAAGC
TTTCTAATCAGCCACAGTTTTGCTGCCAAAACCTTTAACGTCTAGTTCCAATGACGATACA
CTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCTTCATGGAGTTTTTAAACGAT
TTCGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCATTTAACCCCTACCT
CAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAGCAGATTTACAA
TCTGATATTGCTCAGAGTTTTCCGTTCACTCAATTCCAAACATTTCATTACGGCCTTTCCA
TGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTCCCCAACACTTC
ATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCCAAAAAACTCC
GTTTCCAATTCTGTTCCTTTCTCGACAGCGAACGCAGGCCAGTCCATGATTTCCATGGCT
AATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTCTTCTTCAACATCCAGA
ACTAGTCAATCACAGAATGGTGCCCA

FIG. 33

YLR042C Protein Sequence:

**MKISQFGSLAFAPIVLLQLFIVQAQLLTDSNAQDLNTALGQKVQYTFLDTGNSNDQLLHL
PSTTSSSIITGSLAAANFTGSSSSSSIPKVTSSVITSINYQSSNSTVVTQFTPLPSSSRN
ETKSSQTTNTISSSTSTGGVGSVKPCLYFVLMLETIAYLFS**

FIG. 34

SVS1 (YPL163C) DNA Sequence (including 1000 bp upstream and 1000 bp downstream of start and stop codons, respectively):

ATTCTTTGGTTGTGCTTATACATAATTGAAAAAGTGCTAAAATCCTTACACTTCCAAAAC
ATTGAAAGTGGTAATTATTTTCCATCTAAAACCGTTGGGAGCCACCCAGAAAACCCCTTA
TTCTCTGCCTTCGTGAAACAGCTGCTTATATTCATTGTTGGGCTGGGCGTGATGAAGTTC
TGCGTGTCTTAATACTAACTACTTAGAAGACTTGGCATACTGGTTCGCCGATCTTATC
CTTGGCTGGTCAGATTTCATGGCCAACTTTCAAGTTTTTCTGGTCATGTTTGTCTTTCTT
ATCTTACTGAATTGCTTCCAGTACTTTTGTGTCGACAATGTCATCAGGTTACATTCTGAG
AGCCTAACGATAACCAATGCAGAGAATTTTGAAACGAACACATTCTTAAATGACGAAATT
CCTGATTTATCGGAAGTCTCAAATGAAGTGCCTAACAAGGATAACAACATTTCCAGCTAT
GGTAGCATAATATAGTATTCCAAGGATAAGGAAAGCATGCACTGTTTATTTTCCTTTCTT
GCTTAATTGATTTTTTTTTAAAGGGAACAAACATTTTGATTTCAATTTCCACAAGCCTAGA
CTCTTCAACACATAATCTGTGGGTTATTGTTTGGGAAAGCATTCTCCGCTAGAAGAATGA
AAGTGGCGCTCAGGTTTGATTCTATACTACGGCAGTTTTCTTCTATTCTATTTTCGTTTT
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CTTAAGTAATTTCTGTGTTTCAAATAACCGTAAACAGAGAAAAGACCCAAGAATTTTCAGATG
GCTTAGAAGAGGTAGACATTAAATCAATCTGTATGTGATGGAGAGGGAGTGATTTAAAA
GACGTAAGAAAATGAATTATCAAGATCCGTTATGGCCATCTAGTCTCTTTCTTGTACACT
AGTTGTCTAACACAACCAACAAATTAGAATATATATCGCAATGATTTTCAAATATTTGTG
TAGTTTACTACTGGTAACCTCCAACCTTCGCTTCTGCCTTATATGTCAATGAAACTACGAG
CTATACACCATACACGAAGACATTAACCTCAACATACTCTGTTTCACCTCAAGAGACAAC
ATTAACGTACAGCGATGAAACAACCACCTTCTACATAACATCTACTTTTTACTCTACCTA
CTGGTTCACTACCTCCCAATCAGCTGCTATTATTAGTACACCTACTGCAAGTACACCTAC
TGCAAGCACGCTAGCCTAAGTACGCTCCACAAATGAATACACCACCACCTATTCTGACAC
AGACACCACCTACAGCTCTACTCTGACCTCTACTTACATAATAACTCTATCTACGGAATC
CGCCAACGAGAAGGCTGAACAGATTTCCACGAGCGTCACAGAAATTGCTTCTACAGTAAC
CGAATCGGGCAGTACATACACCTCTACTTTGACCTCAACCTTATTGGTTACTGTATATAA
TTCCCAAGCTAGTAATACAATAGCGACATCCACAGCTGGGGACGCCGCTCCAATGTTGA
TGCCTTAGAAAAGTTAGTCTCTGCTGAACATCAATCTCAGATGATTCAAACCACATCCGC
CGATGAACAGTACTGTAGTGCGTCTACCAAGTATGTTACAGTTACAGCTGCTGCAGTTAC
CGAAGTGGTTACTACTACGGCGGAGCCTGTTGTTAAATACGTTACTATAACTGCCGATGC
TAGTAATGTTACAGGTTCTGCTAACCAACGGTACCCACATTTAATGCGTGACGTTGAATCG
AGAAAAAAGCTACTTTTAACGAAACCTTTACTAGTTATCCTATATGGGATCACTAGTAT
TTTTTGATTTACGATTCAATAAATAGACTAGAGACAACCTTTCATATCATTCCTTAAAAAA
TACATAAAGCGCAAATTCACCCCAATTGATACATATATAAGTAGTTCTATTATGACTTTC
AAGAACAATAGTAGCTTTTCTAAATAATCAATAAGTAGCACAAAATCTGTCTGTTTGTAC
GCTTATATTTAGTTTTCGTTTTATTTGCGAGCGCCACGAGAAGGGGCAGGAAAAAAGATC
AATAGTTTGAATAAACATCGAATGATGATTTCAACCACCGATACATAAACCAGCGAGGC
TTTCAAGGAAGAATGAACGTGAACCTCGTCAACTCAAAAAGAAAATGAGCCAGCATATTAG
GAAATTAGATTCTGATGTTTCTGAAAGACTTAAATCTCAGGCATGCACGGTATCGCTAGC
ATCAGCGGTTAGAGAAAATAGTTCAAAATCTGTAGATGCACACGCTACCACTATCGACGT
CATGATCGACCTCCCTAATTTGAGCTTTGCAGTTTACGATGATGGTATTGGTTTGACTCG
AAGTGACCTAAATATATTGGCCACACAAAATTATACTTCCAAAATACGAAAGATGAATGA
TTTAGTAACGATGAAAACCTACGGTTACAGAGGAGACGCCCTATATAGCATTCTAATGT
CTCTAATCTGTTTGTGTTTCCAAAGAAAAAGGATTACAACCTCTGCATGGATGAGAAAATT
TCCATCCAAAAGCGTCATGTTGAGTGAGAATACCATACTCCCAATAGATCCTTTTTGGAA
AATTTGTCTTGGAGCCGAACAAAGTCTGGTACTGTTGTTATTGTTGAAGATATGCTGTA
TAATTTACCTGTCCGGCGCAGAATACTAAAGGAAGAACCCCTTTCAAGACTTTTAACAC
AATAAAGGCAGATATGCTACAGA

FIG. 35

SVS1 (YPL163C) Protein Sequence:

MIFKILCSLLLVTSNFAALYVNETTSYTPYTKLTPTYSVSPQETTLTYSDETTTFYIT
STFYSTYWFTTSQSAAIISTPTASTPTASTPSLTTSTNEYTTTYSDDTTYTSTLTSTYI
ITLSTESANEKAEQISTSVTEIASTVTESGSTYTSTLTSTLLVTVYNSQASNTIATSTAG
DAASNVDALKLVSAEHQSQMIQTTSADQYCSASTKYVTVTAAAVTEVVTTTAEPVVKY
VTITADASNVTGSANNGTHI

FIG. 36

SEQUENCE LISTING

<110> Rosetta Inpharmatics, Inc.

<120> METHODS FOR IDENTIFYING PATHWAY-SPECIFIC REPORTERS AND
TARGET GENES, AND USES THEREOF

<130> 9301-040-228

<140>

<141> 2000-03-29

<150> 09/282,243

<151> 1999-03-31

<160> 30

<170> PatentIn Ver. 2.0

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<213> *Saccharomyces cerevisiae*

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tatcggttgt aaaggagaaa gtatgggtctc tctattttta ttttattaac gaaaaatact 240
aaacgccgat ggggattact atataattat aatagtattt gcagaatagt agaattcttt 300
tcacagttca cgttcagttt ctctctgtgt ttatcgaacg tttattcatc atg tcc      356
                                     Met Ser
                                     1

aag gtc tat ctg aat tca gac atg att aac cat ttg aac tcc aca gtt      404
Lys Val Tyr Leu Asn Ser Asp Met Ile Asn His Leu Asn Ser Thr Val
      5              10              15

caa gct tac ttt aac tta tgg ttg gag aag caa aac gca ata atg cgt      452
Gln Ala Tyr Phe Asn Leu Trp Leu Glu Lys Gln Asn Ala Ile Met Arg
      20              25              30

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 35 40 45 50

acg cta gtt gcc tca att ttc act ctg tat gtt ttg gtc aag ata atc 548
 Thr Leu Val Ala Ser Ile Phe Thr Leu Tyr Val Leu Val Lys Ile Ile
 55 60 65

tcc acc cca gca aag tgt tcc tcg tcc tat aag cca gtc aaa ttc tcc 596
 Ser Thr Pro Ala Lys Cys Ser Ser Ser Tyr Lys Pro Val Lys Phe Ser
 70 75 80

ctt cct gca cca gag gcc gct caa aat aat tgg aag ggc aag agg tct 644
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 85 90 95

gtt tcc act aac ata tgg aat cct gaa gaa cca aac ttt att caa tgt 692
 Val Ser Thr Asn Ile Trp Asn Pro Glu Glu Pro Asn Phe Ile Gln Cys
 100 105 110

cat tgt ccc gcc aca ggt caa tat cta ggt tct ttt cca tcg aaa acg 740
 His Cys Pro Ala Thr Gly Gln Tyr Leu Gly Ser Phe Pro Ser Lys Thr
 115 120 125 130

gaa gct gac ata gat gaa atg gtt tct aag gca ggc aaa gct caa tct 788
 Glu Ala Asp Ile Asp Glu Met Val Ser Lys Ala Gly Lys Ala Gln Ser
 135 140 145

act tgg ggc aat tct gat ttc tca aga aga ttg aga gtt ttg gct tct 836
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 150 155 160

ttg cat gat tat att cta aat aat caa gat ctt att gcg aga gta gcg 884
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 165 170 175

tgc agg gat tca gga aag aca atg tta gac gca tcg atg ggt gaa atc 932
 Cys Arg Asp Ser Gly Lys Thr Met Leu Asp Ala Ser Met Gly Glu Ile
 180 185 190

ttg gtt act tta gaa aaa att caa tgg act ata aag cac ggc caa aga 980
 Leu Val Thr Leu Glu Lys Ile Gln Trp Thr Ile Lys His Gly Gln Arg
 195 200 205 210

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 Ala Leu Gln Pro Ser Arg Arg Pro Gly Pro Thr Asn Phe Phe Met Lys
 215 220 225

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Ser Ile Val Ser Trp Asn Tyr Pro Phe His Asn Leu Leu Gly Pro Ile	
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att gca gca ttg ttc aca ggg aat gcc att gta gta aaa tgt tca gaa	1172
Ile Ala Ala Leu Phe Thr Gly Asn Ala Ile Val Val Lys Cys Ser Glu	
260 265 270	
caa gtt gtc tgg tct tcg gaa ttt ttc gtc gag ctg atc cgc aaa tgt	1220
Gln Val Val Trp Ser Ser Glu Phe Phe Val Glu Leu Ile Arg Lys Cys	
275 280 285 290	
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tta cct cca act gaa aat gat gat tcc gca aat tat ttc acc tct cat	1316
Leu Pro Pro Thr Glu Asn Asp Asp Ser Ala Asn Tyr Phe Thr Ser His	
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cct ggt ttc aaa cat atc act ttt att ggc agt cag ccc gta gcg cac	1364
Pro Gly Phe Lys His Ile Thr Phe Ile Gly Ser Gln Pro Val Ala His	
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tat att cta aaa tgc gct gcc aaa tca ttg aca ccc gta gtt gtg gag	1412
Tyr Ile Leu Lys Cys Ala Ala Lys Ser Leu Thr Pro Val Val Val Glu	
340 345 350	
ctt ggt ggt aag gat gcg ttt att gtc cta gac tca gct aag aat tta	1460
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gat gct tta tct tct atc atc atg agg ggt act ttc caa tca tcc ggt	1508
Asp Ala Leu Ser Ser Ile Ile Met Arg Gly Thr Phe Gln Ser Ser Gly	
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caa aat tgt att ggt att gag agg gtt att gtc agt aag gaa aat tat	1556
Gln Asn Cys Ile Gly Ile Glu Arg Val Ile Val Ser Lys Glu Asn Tyr	
390 395 400	
gat gat tta gtc aag att ttg aat gac cgt atg act gca aat cca cta	1604
Asp Asp Leu Val Lys Ile Leu Asn Asp Arg Met Thr Ala Asn Pro Leu	
405 410 415	

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 Arg Gln Gly Ser Asp Ile Asp His Leu Glu Asn Val Asp Met Gly Ala
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atg ata tct gac aac aga ttc gat gaa cta gaa gct ttg gtt aaa gat 1700
 Met Ile Ser Asp Asn Arg Phe Asp Glu Leu Glu Ala Leu Val Lys Asp
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 Ala Val Ala Lys Gly Ala Arg Leu Leu Gln Gly Gly Ser Arg Phe Lys
 455 460 465

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 His Pro Lys Tyr Pro Gln Gly His Tyr Phe Gln Pro Thr Leu Leu Val
 470 475 480

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 Asp Val Thr Pro Glu Met Lys Ile Ala Gln Asn Glu Val Phe Gly Pro
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att tta gtc atg atg aaa gct aag aat act gac cat tgt gta caa cta 1892
 Ile Leu Val Met Met Lys Ala Lys Asn Thr Asp His Cys Val Gln Leu
 500 505 510

gcc aac tct gcg cca ttt ggt cta ggt ggt tct gtg ttt ggt gcg gat 1940
 Ala Asn Ser Ala Pro Phe Gly Leu Gly Gly Ser Val Phe Gly Ala Asp
 515 520 525 530

atc aag gaa tgc aat tac gtc gca aat agc cta caa act ggt aat gta 1988
 Ile Lys Glu Cys Asn Tyr Val Ala Asn Ser Leu Gln Thr Gly Asn Val
 535 540 545

gcc att aat gat ttt gct aca ttc tat gtt tgt caa tta cca ttt ggt 2036
 Ala Ile Asn Asp Phe Ala Thr Phe Tyr Val Cys Gln Leu Pro Phe Gly
 550 555 560

ggt atc aat ggt tca ggt tac ggt aaa ttt ggt ggt gaa gaa ggt ctt 2084
 Gly Ile Asn Gly Ser Gly Tyr Gly Lys Phe Gly Gly Glu Glu Gly Leu
 565 570 575

ttg ggt ttg tgc aat gcc aaa agt gtc tgt ttt gat act ttg cct ttt 2132
 Leu Gly Leu Cys Asn Ala Lys Ser Val Cys Phe Asp Thr Leu Pro Phe
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gtc tcc act caa att cca aaa cca tta gac tac cct att cgt aac aat 2180
 Val Ser Thr Gln Ile Pro Lys Pro Leu Asp Tyr Pro Ile Arg Asn Asn
 595 600 605 610

gct aag gct tgg aat ttt gta aag agt ttc atc gta gga gct tat aca 2228
 Ala Lys Ala Trp Asn Phe Val Lys Ser Phe Ile Val Gly Ala Tyr Thr
 615 620 625

aat tcc aca tgg caa aga ata aag tca ctg ttc tct tta gct aaa gaa 2276
 Asn Ser Thr Trp Gln Arg Ile Lys Ser Leu Phe Ser Leu Ala Lys Glu
 630 635 640

gcc agc tagtttactt tagaggaagc aacaaactta tcaataattt ggtatttatt 2332
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<211> 644

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

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Met Arg Ser Gln Pro Gln Ile Ile Gln Asp Asn Gln Lys Leu Ile Gly
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Ile Thr Thr Leu Val Ala Ser Ile Phe Thr Leu Tyr Val Leu Val Lys
 50 55 60

Ile Ile Ser Thr Pro Ala Lys Cys Ser Ser Ser Tyr Lys Pro Val Lys
 65 70 75 80

Phe Ser Leu Pro Ala Pro Glu Ala Ala Gln Asn Asn Trp Lys Gly Lys
 85 90 95

Arg Ser Val Ser Thr Asn Ile Trp Asn Pro Glu Glu Pro Asn Phe Ile
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Gln Cys His Cys Pro Ala Thr Gly Gln Tyr Leu Gly Ser Phe Pro Ser
 115 120 125

Lys Thr Glu Ala Asp Ile Asp Glu Met Val Ser Lys Ala Gly Lys Ala
 130 135 140

Gln Ser Thr Trp Gly Asn Ser Asp Phe Ser Arg Arg Leu Arg Val Leu

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165	170	175	
Val Ala Cys Arg Asp Ser Gly Lys Thr Met Leu Asp Ala Ser Met Gly			
180	185	190	
Glu Ile Leu Val Thr Leu Glu Lys Ile Gln Trp Thr Ile Lys His Gly			
195	200	205	
Gln Arg Ala Leu Gln Pro Ser Arg Arg Pro Gly Pro Thr Asn Phe Phe			
210	215	220	
Met Lys Trp Tyr Lys Gly Ala Glu Ile Arg Tyr Glu Pro Leu Gly Val			
225	230	235	240
Ile Ser Ser Ile Val Ser Trp Asn Tyr Pro Phe His Asn Leu Leu Gly			
245	250	255	
Pro Ile Ile Ala Ala Leu Phe Thr Gly Asn Ala Ile Val Val Lys Cys			
260	265	270	
Ser Glu Gln Val Val Trp Ser Ser Glu Phe Phe Val Glu Leu Ile Arg			
275	280	285	
Lys Cys Leu Glu Ala Cys Asp Glu Asp Pro Asp Leu Val Gln Leu Cys			
290	295	300	
Tyr Cys Leu Pro Pro Thr Glu Asn Asp Asp Ser Ala Asn Tyr Phe Thr			
305	310	315	320
Ser His Pro Gly Phe Lys His Ile Thr Phe Ile Gly Ser Gln Pro Val			
325	330	335	
Ala His Tyr Ile Leu Lys Cys Ala Ala Lys Ser Leu Thr Pro Val Val			
340	345	350	
Val Glu Leu Gly Gly Lys Asp Ala Phe Ile Val Leu Asp Ser Ala Lys			
355	360	365	
Asn Leu Asp Ala Leu Ser Ser Ile Ile Met Arg Gly Thr Phe Gln Ser			
370	375	380	
Ser Gly Gln Asn Cys Ile Gly Ile Glu Arg Val Ile Val Ser Lys Glu			
385	390	395	400
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7

<210> 3

<211> 1944

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (801) .. (1841)

<400> 3

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gcaagattca cgaaaccgcg cctcgtttgg accccgaagg cccatttaac ggccggccgt 240
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gcatatagca gttataacag ataaatggca cttttcgcac acccgttggt ttatctccga 660
tagtacgtgg gcctttatatt atggtcgttt aacgaaagaa cggcatcttg aattgagcag 720
gtatttataaa gataggacga gaaacaagca catgatctgt gtcgaaaaaa agtagcaaag 780
agaaaaagta ggaggatagg atg aac agg aaa gta gct atc gta acg ggt act 833
          Met Asn Arg Lys Val Ala Ile Val Thr Gly Thr
                1             5             10

aat agt aat ctt ggt ctg aac att gtg ttc cgt ctg att gaa act gag 881.
Asn Ser Asn Leu Gly Leu Asn Ile Val Phe Arg Leu Ile Glu Thr Glu
          15             20             25

gac acc aat gtc aga ttg acc att gtg gtg act tct aga acg ctt cct 929
Asp Thr Asn Val Arg Leu Thr Ile Val Val Thr Ser Arg Thr Leu Pro
          30             35             40

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cga gtg cag gag gtg att aac cag att aaa gat ttt tac aac aaa tca 977
 Arg Val Gln Glu Val Ile Asn Gln Ile Lys Asp Phe Tyr Asn Lys Ser
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ggc cgt gta gag gat ttg gaa ata gac ttt gat tat ctg ttg gtg gac 1025
 Gly Arg Val Glu Asp Leu Glu Ile Asp Phe Asp Tyr Leu Leu Val Asp
 60 65 70 75

ttc acc aac atg gtg agt gtc ttg aac gca tat tac gac atc aac aaa 1073
 Phe Thr Asn Met Val Ser Val Leu Asn Ala Tyr Tyr Asp Ile Asn Lys
 80 85 90

aag tac agg gcg ata aac tac ctt ttc gtg aat gct gcg caa ggt atc 1121
 Lys Tyr Arg Ala Ile Asn Tyr Leu Phe Val Asn Ala Ala Gln Gly Ile
 95 100 105

ttt gac ggt ata gat tgg atc gga gcg gtc aag gag gtt ttc acc aat 1169
 Phe Asp Gly Ile Asp Trp Ile Gly Ala Val Lys Glu Val Phe Thr Asn
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cca ttg gag gca gtg aca aat ccg aca tac aag ata caa ctg gtg ggc 1217
 Pro Leu Glu Ala Val Thr Asn Pro Thr Tyr Lys Ile Gln Leu Val Gly
 125 130 135

gtc aag tct aaa gat gac atg ggg ctt att ttc cag gcc aat gtg ttt 1265
 Val Lys Ser Lys Asp Asp Met Gly Leu Ile Phe Gln Ala Asn Val Phe
 140 145 150 155

ggt ccg tac tac ttt atc agt aaa att ctg cct caa ttg acc agg gga 1313
 Gly Pro Tyr Tyr Phe Ile Ser Lys Ile Leu Pro Gln Leu Thr Arg Gly
 160 165 170

aag gct tat att gtt tgg att tcg agt att atg tcc gat cct aag tat 1361
 Lys Ala Tyr Ile Val Trp Ile Ser Ser Ile Met Ser Asp Pro Lys Tyr
 175 180 185

ctt tcg ttg aac gat att gaa cta cta aag aca aat gcc tct tat gag 1409
 Leu Ser Leu Asn Asp Ile Glu Leu Leu Lys Thr Asn Ala Ser Tyr Glu
 190 195 200

ggc tcc aag cgt tta gtt gat tta ctg cat ttg gcc acc tac aaa gac 1457
 Gly Ser Lys Arg Leu Val Asp Leu Leu His Leu Ala Thr Tyr Lys Asp
 205 210 215

ttg aaa aag ctg ggc ata aat cag tat gta gtt caa ccg ggc ata ttt 1505
 Leu Lys Lys Leu Gly Ile Asn Gln Tyr Val Val Gln Pro Gly Ile Phe
 220 225 230 235

aca agc cat tcc ttc tcc gaa tat ttg aat ttt ttc acc tat ttc ggc 1553
 Thr Ser His Ser Phe Ser Glu Tyr Leu Asn Phe Phe Thr Tyr Phe Gly
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atg cta tgc ttg ttc tat ttg gcc agg ctg ttg ggg tct cca tgg cac 1601
 Met Leu Cys Leu Phe Tyr Leu Ala Arg Leu Leu Gly Ser Pro Trp His
 255 260 265

aat att gat ggt tat aaa gct gcc aat gcc cca gta tac gta act aga 1649
 Asn Ile Asp Gly Tyr Lys Ala Ala Asn Ala Pro Val Tyr Val Thr Arg
 270 275 280

ttg gcc aat cca aac ttt gag aaa caa gac gta aaa tac ggt tct gct 1697
 Leu Ala Asn Pro Asn Phe Glu Lys Gln Asp Val Lys Tyr Gly Ser Ala
 285 290 295

acc tct agg gat ggt atg cca tat atc aag acg cag gaa ata gac cct 1745
 Thr Ser Arg Asp Gly Met Pro Tyr Ile Lys Thr Gln Glu Ile Asp Pro
 300 305 310 315

act gga atg tct gat gtc ttc gct tat ata cag aag aag aaa ctg gaa 1793
 Thr Gly Met Ser Asp Val Phe Ala Tyr Ile Gln Lys Lys Lys Leu Glu
 320 325 330

tgg gac gag aaa ctg aaa gat caa att gtt gaa act aga acc ccc att 1841
 Trp Asp Glu Lys Leu Lys Asp Gln Ile Val Glu Thr Arg Thr Pro Ile
 335 340 345

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atagaaaacg catatcaact gatatatata cacgtgaagc aaa 1944

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<211> 347

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

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Leu Thr Ile Val Val Thr Ser Arg Thr Leu Pro Arg Val Gln Glu Val

35 40 45

Ile Asn Gln Ile Lys Asp Phe Tyr Asn Lys Ser Gly Arg Val Glu Asp
 50 55 60

Leu Glu Ile Asp Phe Asp Tyr Leu Leu Val Asp Phe Thr Asn Met Val
 65 70 75 80

Ser Val Leu Asn Ala Tyr Tyr Asp Ile Asn Lys Lys Tyr Arg Ala Ile
 85 90 95

Asn Tyr Leu Phe Val Asn Ala Ala Gln Gly Ile Phe Asp Gly Ile Asp
 100 105 110

Trp Ile Gly Ala Val Lys Glu Val Phe Thr Asn Pro Leu Glu Ala Val
 115 120 125

Thr Asn Pro Thr Tyr Lys Ile Gln Leu Val Gly Val Lys Ser Lys Asp
 130 135 140

Asp Met Gly Leu Ile Phe Gln Ala Asn Val Phe Gly Pro Tyr Tyr Phe
 145 150 155 160

Ile Ser Lys Ile Leu Pro Gln Leu Thr Arg Gly Lys Ala Tyr Ile Val
 165 170 175

Trp Ile Ser Ser Ile Met Ser Asp Pro Lys Tyr Leu Ser Leu Asn Asp
 180 185 190

Ile Glu Leu Leu Lys Thr Asn Ala Ser Tyr Glu Gly Ser Lys Arg Leu
 195 200 205

Val Asp Leu Leu His Leu Ala Thr Tyr Lys Asp Leu Lys Lys Leu Gly
 210 215 220

Ile Asn Gln Tyr Val Val Gln Pro Gly Ile Phe Thr Ser His Ser Phe
 225 230 235 240

Ser Glu Tyr Leu Asn Phe Phe Thr Tyr Phe Gly Met Leu Cys Leu Phe
 245 250 255

Tyr Leu Ala Arg Leu Leu Gly Ser Pro Trp His Asn Ile Asp Gly Tyr
 260 265 270

Lys Ala Ala Asn Ala Pro Val Tyr Val Thr Arg Leu Ala Asn Pro Asn
 275 280 285

Phe Glu Lys Gln Asp Val Lys Tyr Gly Ser Ala Thr Ser Arg Asp Gly
 290 295 300

Met Pro Tyr Ile Lys Thr Gln Glu Ile Asp Pro Thr Gly Met Ser Asp
 305 310 315 320

Val Phe Ala Tyr Ile Gln Lys Lys Lys Leu Glu Trp Asp Glu Lys Leu
 325 330 335

Lys Asp Gln Ile Val Glu Thr Arg Thr Pro Ile
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<210> 5

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<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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<222> (1001) .. (2551)

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 gtaataggag tatattgaac gacaccgggt caacaagcaa ctttcctaag cctttttacac 180
 ttctttcacat cattcaagat cgccttttaa cgagctacaa accttcacgt tcgttcttct 240
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 agccacctta acgtctactt agagccttag aaaagccatc aagattgggtg gaatagttgt 420
 tgagggaact tagccgccac attctcgtag ccaaataaag cgaatctgac cattgtatgt 480
 ttcttttttca ctggtatgat agcccaatgt gttaaggaa agttaggaca acacacccga 540
 agaaggacgt cacccttgca ttcccaaagc agctatgaaa tagctctttc ctctacaagt 600
 aataacaaca acttttttgt ctgttttccg accgtttaac ttcagagatt aattttttca 660
 acgcgctttc gttgaacgtc gcaaattcgt ttagaataaa cgaaagggtga cagaaataga 720
 agattatagc catgcatacg cacataaatt gaaaactgtt tcgaggctga gtattccctg 780
 cgtctgcagc catcaggggt atgactctgc tacacgttta ctatattctt ggctaaacga 840

13

gat ata ttt tca gca gct aac ttt cac aaa tta ttt tta aaa gag tta	1543
Asp Ile Phe Ser Ala Ala Asn Phe His Lys Leu Phe Leu Lys Glu Leu	
170 175 180	
aac gaa atc agc aca gta aca cac tct gaa gat agg att ttg ttt gat	1591
Asn Glu Ile Ser Thr Val Thr His Ser Glu Asp Arg Ile Leu Phe Asp	
185 190 195	
gtc aat gac atc aat ctc tca gaa tta aaa ttt ccc aaa tcg ata tat	1639
Val Asn Asp Ile Asn Leu Ser Glu Leu Lys Phe Pro Lys Ser Ile Tyr	
200 205 210	
gat agc gca aaa tta cac ctg ccc gct atg aca cca caa atc ttc cac	1687
Asp Ser Ala Lys Leu His Leu Pro Ala Met Thr Pro Gln Ile Phe His	
215 220 225	
aag caa act cag tca ttt ttc aaa tca ata tac tat aac act tta aaa	1735
Lys Gln Thr Gln Ser Phe Phe Lys Ser Ile Tyr Tyr Asn Thr Leu Lys	
230 235 240 245	
aga cct ttc ggc tat tta acc aat caa act tcc ctc agc tcg tca gta	1783
Arg Pro Phe Gly Tyr Leu Thr Asn Gln Thr Ser Leu Ser Ser Val	
250 255 260	
tct gca aca cag ctg aaa aag tat aat gat att cta aat gcg cac acc	1831
Ser Ala Thr Gln Leu Lys Lys Tyr Asn Asp Ile Leu Asn Ala His Thr	
265 270 275	
tca tta tgc ggg aca aca gta ttt ggg ata gta aac aac caa agg ttt	1879
Ser Leu Cys Gly Thr Thr Val Phe Gly Ile Val Asn Asn Gln Arg Phe	
280 285 290	
aac tat tta aag tca atc gtt aat caa gag cat ata tgt cta aga agt	1927
Asn Tyr Leu Lys Ser Ile Val Asn Gln Glu His Ile Cys Leu Arg Ser	
295 300 305	
ttc atc tgt ggt att gca atg ata tgt tta aaa cct ctc gtt aag gat	1975
Phe Ile Cys Gly Ile Ala Met Ile Cys Leu Lys Pro Leu Val Lys Asp	
310 315 320 325	
ttc agc ggt aca ata gta ttt act att ccc ata aat tta aga aac cac	2023
Phe Ser Gly Thr Ile Val Phe Thr Ile Pro Ile Asn Leu Arg Asn His	
330 335 340	
tta ggc tta ggt ggg tca ttg ggt ctc ttc ttc aaa gaa cta agg gtc	2071
Leu Gly Leu Gly Ser Leu Gly Leu Phe Phe Lys Glu Leu Arg Val	
345 350 355	

gaa tgt cca ctt tct cta att gat gac gaa ctt tcc gcc aac gaa ttt 2119
 Glu Cys Pro Leu Ser Leu Ile Asp Asp Glu Leu Ser Ala Asn Glu Phe
 360 365 370

ttg acc aac agt aac gat aac gag gat aat gat gat gag ttt aat gaa 2167
 Leu Thr Asn Ser Asn Asp Asn Glu Asp Asn Asp Asp Glu Phe Asn Glu
 375 380 385

aga ttg atg gaa tat caa ttt aat aaa gtt aca aag cac gtt agc ggt 2215
 Arg Leu Met Glu Tyr Gln Phe Asn Lys Val Thr Lys His Val Ser Gly
 390 395 400 405

ttt att atg gca aaa ctg agg agt tgg gaa aag aat ggg ttt aat gat 2263
 Phe Ile Met Ala Lys Leu Arg Ser Trp Glu Lys Asn Gly Phe Asn Asp
 410 415 420

gac gat ata agg agg atg aag tat gac aat gac gac gat ttc cat atc 2311
 Asp Asp Ile Arg Arg Met Lys Tyr Asp Asn Asp Asp Asp Phe His Ile
 425 430 435

caa aat tca agg aca aaa ttg att caa atc aat gat gtt tcc gac ata 2359
 Gln Asn Ser Arg Thr Lys Leu Ile Gln Ile Asn Asp Val Ser Asp Ile
 440 445 450

tcg tta tcg atg aac ggc gat gac aaa tct ttc aaa att gta agt acg 2407
 Ser Leu Ser Met Asn Gly Asp Asp Lys Ser Phe Lys Ile Val Ser Thr
 455 460 465

gga ttt aca agt tcg ata aat cgc ccc aca tta atg tct ctt tcc tat 2455
 Gly Phe Thr Ser Ser Ile Asn Arg Pro Thr Leu Met Ser Leu Ser Tyr
 470 475 480 485

aca tac tgt gaa gag atg ggc ctg aat atc tgt att cac tac cct gat 2503
 Thr Tyr Cys Glu Glu Met Gly Leu Asn Ile Cys Ile His Tyr Pro Asp
 490 495 500

tcg tat aat tta gaa tct ttt gta gaa tgc ttc gaa tcc ttt att gaa 2551
 Ser Tyr Asn Leu Glu Ser Phe Val Glu Cys Phe Glu Ser Phe Ile Glu
 505 510 515

taggcaggtg acgcattaaa tatatgtctg tatagtacgt attttttcca ttttatttat 2611

tcttatcaaaa atttaaatcaa catatatgct aaagaaacta ttgataggag atatgacagg 2671

aaattgcact gtttctggaa ctttggcatg ccgaggccgt catttccagt ataactgagc 2731

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<211> 517

<212> PRT

<213> *Saccharomyces cerevisiae*

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Ser Lys Ser Leu Ser Arg Glu Asn Asp Ala Asp Trp His Ser Asp Glu
 35 40 45

Val Thr Leu Gly Thr Asn Ser Ser Lys Asp Asp Ser Arg Leu Thr Leu
 50 55 60

Pro Leu Ile Ala Thr Thr Leu Lys Arg Leu Ile Lys Ser Gln Pro Ala
 65 70 75 80

Leu Phe Ala Thr Val Asn Glu Glu Trp Glu Phe Glu Pro Leu Lys Gln
 85 90 95

Leu Lys Thr Ser Asp Ile Val Asn Val Ile Glu Phe Glu Thr Ile Lys
 100 105 110

Asp Lys Glu Val Asn Cys His Trp Gly Val Pro Pro Pro Tyr Leu Leu
 115 120 125

Arg His Ala Phe Asn Lys Thr Arg Phe Val Pro Gly Ser Asn Lys Pro
 130 135 140

Leu Trp Thr Leu Tyr Val Ile Asp Glu Ala Leu Leu Val Phe His Gly
 145 150 155 160

His Asp Val Leu Phe Asp Ile Phe Ser Ala Ala Asn Phe His Lys Leu
 165 170 175

Phe Leu Lys Glu Leu Asn Glu Ile Ser Thr Val Thr His Ser Glu Asp
 180 185 190

Arg Ile Leu Phe Asp Val Asn Asp Ile Asn Leu Ser Glu Leu Lys Phe
 195 200 205

Pro Lys Ser Ile Tyr Asp Ser Ala Lys Leu His Leu Pro Ala Met Thr
 210 215 220

Pro Gln Ile Phe His Lys Gln Thr Gln Ser Phe Phe Lys Ser Ile Tyr
 225 230 235 240

Tyr Asn Thr Leu Lys Arg Pro Phe Gly Tyr Leu Thr Asn Gln Thr Ser
 245 250 255

Leu Ser Ser Ser Val Ser Ala Thr Gln Leu Lys Lys Tyr Asn Asp Ile
 260 265 270

Leu Asn Ala His Thr Ser Leu Cys Gly Thr Thr Val Phe Gly Ile Val
 275 280 285

Asn Asn Gln Arg Phe Asn Tyr Leu Lys Ser Ile Val Asn Gln Glu His
 290 295 300

Ile Cys Leu Arg Ser Phe Ile Cys Gly Ile Ala Met Ile Cys Leu Lys
 305 310 315 320

Pro Leu Val Lys Asp Phe Ser Gly Thr Ile Val Phe Thr Ile Pro Ile
 325 330 335

Asn Leu Arg Asn His Leu Gly Leu Gly Gly Ser Leu Gly Leu Phe Phe
 340 345 350

Lys Glu Leu Arg Val Glu Cys Pro Leu Ser Leu Ile Asp Asp Glu Leu
 355 360 365

Ser Ala Asn Glu Phe Leu Thr Asn Ser Asn Asp Asn Glu Asp Asn Asp
 370 375 380

Asp Glu Phe Asn Glu Arg Leu Met Glu Tyr Gln Phe Asn Lys Val Thr
 385 390 395 400

Lys His Val Ser Gly Phe Ile Met Ala Lys Leu Arg Ser Trp Glu Lys
 405 410 415

Asn Gly Phe Asn Asp Asp Asp Ile Arg Arg Met Lys Tyr Asp Asn Asp
 420 425 430

Asp Asp Phe His Ile Gln Asn Ser Arg Thr Lys Leu Ile Gln Ile Asn
 435 440 445

Asp Val Ser Asp Ile Ser Leu Ser Met Asn Gly Asp Asp Lys Ser Phe
 450 455 460

Lys Ile Val Ser Thr Gly Phe Thr Ser Ser Ile Asn Arg Pro Thr Leu
 465 470 475 480

Met Ser Leu Ser Tyr Thr Tyr Cys Glu Glu Met Gly Leu Asn Ile Cys
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<210> 7

<211> 1725

<212> DNA

<213> *Saccharomyces cerevisiae*

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<221> CDS

<222> (1001) .. (1522)

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 aagatgtacg aggggtccacg gggtagcaag cacaagaacg atgatataata tgacagaacg 240
 atggataaga atggatatgtt gtctgcactg ttcagcattc gactaccctt cttccgggtt 300
 ttttctcttc gtttcaattt aaaaaagcaa ctgctaccc ggccgcacac cccttattcc 360
 tgttcagccg ttttaagggtga gaacccttta cttcatagcc tttgtagatc tttctattgc 420
 taccattgaa gggtcgggtga cgtggaaatt ttgacattta tcagtggcgt attgggaggc 480
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 tttcctttac gaacaatgag caatgttttg cacaggcagg tgggaagtag ggcctatcgc 840

gccttggatg cagatataag tataaatata aattataata attggctgta tcagtaaattc 900

cttcttgcca tgggaggaag cacgatagag tatgttaagc ttttgagagg cttcatattc 960

attggaattt taaataacaa taaagcaaca acaataataa atg cta tca gct gca 1015
Met Leu Ser Ala Ala
1 5

gat aat tta gtg cgc atc ata aat gct gtt ttt ctt att ata tcc ata 1063
Asp Asn Leu Val Arg Ile Ile Asn Ala Val Phe Leu Ile Ile Ser Ile
10 15 20

ggt cta atc agc ggc ctg ata ggt aca cag aca aag cat agt tct cga 1111
Gly Leu Ile Ser Gly Leu Ile Gly Thr Gln Thr Lys His Ser Ser Arg
25 30 35

gtg aac ttt tgt atg ttt gcc gcc gtt tat ggt ctg gtt acg gat tca 1159
Val Asn Phe Cys Met Phe Ala Ala Val Tyr Gly Leu Val Thr Asp Ser
40 45 50

tta tat ggg ttt ttg gct aat ttc tgg aca tca tta aca tac cca gca 1207
Leu Tyr Gly Phe Leu Ala Asn Phe Trp Thr Ser Leu Thr Tyr Pro Ala
55 60 65

att ttg ctt gtt ttg gat ttt tta aat ttc ata ttt acg ttt gta gca 1255
Ile Leu Leu Val Leu Asp Phe Leu Asn Phe Ile Phe Thr Phe Val Ala
70 75 80 85

gcc acc gct ttg gct gta ggt ata aga tgc cat tcg tgt aaa aac aaa 1303
Ala Thr Ala Leu Ala Val Gly Ile Arg Cys His Ser Cys Lys Asn Lys
90 95 100

aca tat ctg gaa cag aat aag atc ata caa ggc tca agc tcc aga tgt 1351
Thr Tyr Leu Glu Gln Asn Lys Ile Ile Gln Gly Ser Ser Ser Arg Cys
105 110 115

cat caa tct cag gct gct gtt gcg ttt ttt tac ttt tcc tgt ttt cta 1399
His Gln Ser Gln Ala Ala Val Ala Phe Phe Tyr Phe Ser Cys Phe Leu
120 125 130

ttc ctc atc aaa gtg act gtg gcc acg atg ggt atg atg caa aat ggt 1447
Phe Leu Ile Lys Val Thr Val Ala Thr Met Gly Met Met Gln Asn Gly
135 140 145

gga ttt ggc tct aat acc gga ttc agc aga agg agg gca aga aga caa 1495
Gly Phe Gly Ser Asn Thr Gly Phe Ser Arg Arg Arg Ala Arg Arg Gln
150 155 160 165

atg ggc ata cct aca att tcc cag gtt taagcctact ggactgaaaa 1542
Met Gly Ile Pro Thr Ile Ser Gln Val

170

aaaggcaatt cgcgtacaat tttcgttgat cgttctttat ataacctttg cattaaataa 1602

atttaacaaa aaaagttctt tctaaaataa tattatgggtg atacatgaat gtgcttttagt 1662

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<211> 174

<212> PRT

<213> *Saccharomyces cerevisiae*

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Lys His Ser Ser Arg Val Asn Phe Cys Met Phe Ala Ala Val Tyr Gly
35 40 45

Leu Val Thr Asp Ser Leu Tyr Gly Phe Leu Ala Asn Phe Trp Thr Ser
50 55 60

Leu Thr Tyr Pro Ala Ile Leu Leu Val Leu Asp Phe Leu Asn Phe Ile
65 70 75 80

Phe Thr Phe Val Ala Ala Thr Ala Leu Ala Val Gly Ile Arg Cys His
85 90 95

Ser Cys Lys Asn Lys Thr Tyr Leu Glu Gln Asn Lys Ile Ile Gln Gly
100 105 110

Ser Ser Ser Arg Cys His Gln Ser Gln Ala Ala Val Ala Phe Phe Tyr
115 120 125

Phe Ser Cys Phe Leu Phe Leu Ile Lys Val Thr Val Ala Thr Met Gly
130 135 140

Met Met Gln Asn Gly Gly Phe Gly Ser Asn Thr Gly Phe Ser Arg Arg

Arg Ala Arg Arg Gln Met Gly Ile Pro Thr Ile Ser Gln Val
165 170

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<221> CDS
<222> (1001) .. (1588)
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gccagggtttt tgtttattgc tccaccatcg gtcgaggatt tgaaaaaaag attagaagggt 240
agagggtacgg agaccgaaga atccatcaac aagagggttaa gcgccgctca agctgaattg 300
gcatatgctg agacagggtgc ccatgacaaa gttattgtca atgatgattt ggacaaggcc 360
tacaaggaat tgaaggattt tatctttgca gaaaaatgat gttagcctat atagacatta 420
ctaagtatgt acctggtagg agagtgtgtg cgcaaagcga caaacgctcc aattattcaa 480
ttaatatagt gtaaaagttc tcaacggggt tatgctagtt ttttttgta gtaagcgcta 540
cgacgactag aaccatctct tgaatttcca agtgccaaaa tcaatgacca cggatactgt 600
ggccaggaat ctgttggttg gtcacctca agatctagac aatatcatat tgggccagta 660
tctgattatc ttaactatat gcgcccctct agtttacaag ttttagtcat tggggggttg 720
aagggtgat ccccccttac aattggcgtc gtttaggagc gggcgaggct ctcctttctc 780
ttacacatct gctaagggtg ttgttaccg agtaatcaag gatcaactat ggatgagatt 840
tagattaacg tatttagagc agacgattgt aagaatatat tttgtaattt cgattgtttt 900
ttgctactta cattgtttat cttgaaatat ccaaagtga cactattact gttttttgct 960

22

cct gac gtt aaa gat tcc aag gag tat ttc aaa aat gcc aat aat 1588
 Pro Asp Val Lys Asp Ser Lys Glu Tyr Phe Lys Asn Ala Asn Asn
 185 190 195

taatcttgcg acgataacgc taggcctat taaataatta aaaatacatc accctatata 1648
 tgataagaaa gatggttttg tattattatg aaattgactt gaaagaatag tgtaacaaaa 1708
 gaaaaagaaa ctgtaattga agaattgatat gcatttctat gtgtatatta acttaatcat 1768
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 <212> PRT
 <213> *Saccharomyces cerevisiae*

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 20 25 30

Lys Tyr Val Val Leu Ala Phe Val Pro Leu Ala Phe Ser Phe Val Cys
 35 40 45

Pro Thr Glu Ile Val Ala Phe Ser Asp Ala Ala Lys Lys Phe Glu Asp
 50 55 60

Gln Gly Ala Gln Val Leu Phe Ala Ser Thr Asp Ser Glu Tyr Ser Leu
 65 70 75 80

Leu Ala Trp Thr Asn Leu Pro Arg Lys Asp Gly Gly Leu Gly Pro Val
 85 90 95

Lys Val Pro Leu Leu Ala Asp Lys Asn His Ser Leu Ser Arg Asp Tyr
 100 105 110

Gly Val Leu Ile Glu Lys Glu Gly Ile Ala Leu Arg Gly Leu Phe Ile
 115 120 125

Ile Asp Pro Lys Gly Ile Ile Arg His Ile Thr Ile Asn Asp Leu Ser
 130 135 140

Val Gly Arg Asn Val Asn Glu Ala Leu Arg Leu Val Glu Gly Phe Gln
 145 150 155 160

Trp Thr Asp Lys Asn Gly Thr Val Leu Pro Cys Asn Trp Thr Pro Gly
 165 170 175

Ala Ala Thr Ile Lys Pro Asp Val Lys Asp Ser Lys Glu Tyr Phe Lys
 180 185 190

Asn Ala Asn Asn
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<210> 11

<211> 3455

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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<222> (1001) .. (2452)

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 ttgaatgccca ggccattagc tagattggaa cgtttgaaaa tcttgataaa ctatgcagtt 180
 aagatctctc cgcataagga aaaattcccc tatgtgaggt ggacagtggg taaaaacaag 240
 tacatacatg agctcatggt cccagagcgc tttcccattg atattcccag agaaaatgtc 300
 gggtagaaa gaactcagat tccattaatg ctatgctggg cactgtccat tcataaggca 360
 caggggtcaaa ctattcaaag actaaaggtc gacttgagga gaattttcga agccggccaa 420
 gtttatgttg cactgtcaag agcggtaact atggacacct tacaggtcct aaactttgat 480
 ccaggaaaga ttgcaccaa tgaaagagta aaagatttct ataaacgttt agaaactttg 540
 aaatgacttg caacgaataa atgcatatac tctagttgaa gttttctttt cttgttctat 600
 acagggttcga atacttgtga gcctatctgt ataatttaac agaatcccga aatattcatc 660
 tagaagccat ctatttagct aagcctacgt atgcggcgat ttttatatta tctttttttt 720
 tttttataga agactgcgaa atgttggcag aatggaaagt ttcagtgtta aaaatagaaa 780
 ctgaaaaagg agatctagcc aggaatatat cgaaaaaaaa agtgagggaa atcagatcct 840

acacaaatat ttagatttaa ttgaagaccc tggctcgcca gatatatata tatattagac 900

gaactgtgca ttcagtcagc aaatctaggc cacagatttt cttattgaag ctatcaaaat 960

agtagaaata attgaagggc gtgtataaca attctgggag atg gct gat aag ata 1015
Met Ala Asp Lys Ile
1 5

gag agg cat act ttc aag gtc ttc aat caa gat ttc agt gta gat aag 1063
Glu Arg His Thr Phe Lys Val Phe Asn Gln Asp Phe Ser Val Asp Lys
10 15 20

agg ttt caa ctt atc aaa gaa ata ggg cat gga gca tac ggc ata gtg 1111
Arg Phe Gln Leu Ile Lys Glu Ile Gly His Gly Ala Tyr Gly Ile Val
25 30 35

tgt tca gcg cgg ttt gca gaa gct gcc gaa gat acc aca gtt gcc atc 1159
Cys Ser Ala Arg Phe Ala Glu Ala Ala Glu Asp Thr Thr Val Ala Ile
40 45 50

aag aaa gtg aca aac gtt ttt tcg aag acc tta cta tgt aaa aga tcc 1207
Lys Lys Val Thr Asn Val Phe Ser Lys Thr Leu Leu Cys Lys Arg Ser
55 60 65

cta cgt gag cta aag ctt ttg aga cat ttc aga ggc cac aaa aat att 1255
Leu Arg Glu Leu Lys Leu Leu Arg His Phe Arg Gly His Lys Asn Ile
70 75 80 85

aca tgt ctt tat gat atg gat att gtt ttt tat cca gac ggg tct atc 1303
Thr Cys Leu Tyr Asp Met Asp Ile Val Phe Tyr Pro Asp Gly Ser Ile
90 95 100

aat gga cta tat ctt tat gag gaa ctt atg gaa tgt gat atg cac caa 1351
Asn Gly Leu Tyr Leu Tyr Glu Glu Met Glu Cys Asp Met His Gln
105 110 115

atc atc aaa tcc ggt caa cct ttg acg gat gct cac tat caa agt ttc 1399
Ile Ile Lys Ser Gly Gln Pro Leu Thr Asp Ala His Tyr Gln Ser Phe
120 125 130

aca tac caa ata tta tgt ggt tta aag tat att cat tct gca gat gtc 1447
Thr Tyr Gln Ile Leu Cys Gly Leu Lys Tyr Ile His Ser Ala Asp Val
135 140 145

ttg cat cgt gat ttg aag ccc ggc aat ttg ctt gtc aat gca gat tgt 1495
Leu His Arg Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asp Cys
150 155 160 165

caa ttg aaa atc tgt gat ttt ggg tta gct aga ggt tat tcg gag aat 1543
 Gln Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Tyr Ser Glu Asn
 170 175 180

cct gtc gaa aac agt caa ttt ttg acg gag tac gtg gcc act aga tgg 1591
 Pro Val Glu Asn Ser Gln Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp
 185 190 195

tat aga gct ccg gaa ata atg ttg agt tac caa gga tat acc aag gcg 1639
 Tyr Arg Ala Pro Glu Ile Met Leu Ser Tyr Gln Gly Tyr Thr Lys Ala
 200 205 210

att gac gta tgg tca gct ggc tgt att tta gcg gag ttt ctt ggt gga 1687
 Ile Asp Val Trp Ser Ala Gly Cys Ile Leu Ala Glu Phe Leu Gly Gly
 215 220 225

aag cca atc ttc aaa gga aag gat tac gtt aat caa ttg aat caa ata 1735
 Lys Pro Ile Phe Lys Gly Lys Asp Tyr Val Asn Gln Leu Asn Gln Ile
 230 235 240 245

tta caa gtt tta ggg aca ccc cca gac gaa act tta aga agg att ggt 1783
 Leu Gln Val Leu Gly Thr Pro Pro Asp Glu Thr Leu Arg Arg Ile Gly
 250 255 260

tct aaa aat gtt cag gac tac ata cat caa tta ggt ttc att cca aaa 1831
 Ser Lys Asn Val Gln Asp Tyr Ile His Gln Leu Gly Phe Ile Pro Lys
 265 270 275

gta cct ttt gtc aat tta tac cca aat gcc aat tca caa gca tta gac 1879
 Val Pro Phe Val Asn Leu Tyr Pro Asn Ala Asn Ser Gln Ala Leu Asp
 280 285 290

tta ttg gag caa atg ctc gcg ttt gac cct caa aag aga att acc gtg 1927
 Leu Leu Glu Gln Met Leu Ala Phe Asp Pro Gln Lys Arg Ile Thr Val
 295 300 305

gat gag gcc ctg gag cat cct tac ttg tct ata tgg cat gat cca gct 1975
 Asp Glu Ala Leu Glu His Pro Tyr Leu Ser Ile Trp His Asp Pro Ala
 310 315 320 325

gac gaa cct gtg tgt agt gaa aaa ttc gaa ttt agt ttt gaa tcg gtt 2023
 Asp Glu Pro Val Cys Ser Glu Lys Phe Glu Phe Ser Phe Glu Ser Val
 330 335 340

aat gat atg gag gac tta aaa caa atg gtt ata caa gaa gtg caa gat 2071
 Asn Asp Met Glu Asp Leu Lys Gln Met Val Ile Gln Glu Val Gln Asp
 345 350 355

ttc agg ctg ttt gtg aga caa ccg cta tta gaa gag caa agg caa tta 2119
 Phe Arg Leu Phe Val Arg Gln Pro Leu Leu Glu Glu Gln Arg Gln Leu
 360 365 370

caa tta cag cag cag caa cag cag cag caa cag caa cag caa 2167
 Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 375 380 385

cag cag cct tca gat gtg gat aat ggc aac gcc gca gcg agt gaa gaa 2215
 Gln Gln Pro Ser Asp Val Asp Asn Gly Asn Ala Ala Ala Ser Glu Glu
 390 395 400 405

aat tat cca aaa cag atg gcc acg tct aat tct gtt gcg cca caa caa 2263
 Asn Tyr Pro Lys Gln Met Ala Thr Ser Asn Ser Val Ala Pro Gln Gln
 410 415 420

gaa tca ttt ggt att cac tcc caa aat ttg cca agg cat gat gca gat 2311
 Glu Ser Phe Gly Ile His Ser Gln Asn Leu Pro Arg His Asp Ala Asp
 425 430 435

ttc cca cct cga cct caa gag agt atg atg gag atg aga cct gcc act 2359
 Phe Pro Pro Arg Pro Gln Glu Ser Met Met Glu Met Arg Pro Ala Thr
 440 445 450

gga aat acc gca gat att ccg cct cag aat gat aac ggc acg ctt cta 2407
 Gly Asn Thr Ala Asp Ile Pro Pro Gln Asn Asp Asn Gly Thr Leu Leu
 455 460 465

gac ctt gaa aaa gag ctg gag ttt gga tta gat aga aaa tat ttt 2452
 Asp Leu Glu Lys Glu Leu Glu Phe Gly Leu Asp Arg Lys Tyr Phe
 470 475 480

taggacaaaa aactataagt aaccggggaa gtatagaatc accatagatg taagcttaca 2512

gacaatgtgt atatatgatg tatatgaacg tatacaaata tatatatata tacgtgctct 2572

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gtttgttatc gcctcttgaa ttctttcttt tcgttcattt atgattagtc atctatagac 2692

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<211> 484

<212> PRT

<213> *Saccharomyces cerevisiae*

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20 25 30

Ala Tyr Gly Ile Val Cys Ser Ala Arg Phe Ala Glu Ala Ala Glu Asp

35 40 45

Thr Thr Val Ala Ile Lys Lys Val Thr Asn Val Phe Ser Lys Thr Leu

50 55 60

Leu Cys Lys Arg Ser Leu Arg Glu Leu Lys Leu Leu Arg His Phe Arg

65 70 75 80

Gly His Lys Asn Ile Thr Cys Leu Tyr Asp Met Asp Ile Val Phe Tyr

85 90 95

Pro Asp Gly Ser Ile Asn Gly Leu Tyr Leu Tyr Glu Glu Leu Met Glu

100 105 110

Cys Asp Met His Gln Ile Ile Lys Ser Gly Gln Pro Leu Thr Asp Ala

115	120	125
His Tyr Gln Ser Phe Thr Tyr Gln Ile Leu Cys Gly Leu Lys Tyr Ile		
130	135	140
His Ser Ala Asp Val Leu His Arg Asp Leu Lys Pro Gly Asn Leu Leu		
145	150	155 160
Val Asn Ala Asp Cys Gln Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg		
165	170	175
Gly Tyr Ser Glu Asn Pro Val Glu Asn Ser Gln Phe Leu Thr Glu Tyr		
180	185	190
Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Ser Tyr Gln		
195	200	205
Gly Tyr Thr Lys Ala Ile Asp Val Trp Ser Ala Gly Cys Ile Leu Ala		
210	215	220
Glu Phe Leu Gly Gly Lys Pro Ile Phe Lys Gly Lys Asp Tyr Val Asn		
225	230	235 240
Gln Leu Asn Gln Ile Leu Gln Val Leu Gly Thr Pro Pro Asp Glu Thr		
245	250	255
Leu Arg Arg Ile Gly Ser Lys Asn Val Gln Asp Tyr Ile His Gln Leu		
260	265	270
Gly Phe Ile Pro Lys Val Pro Phe Val Asn Leu Tyr Pro Asn Ala Asn		
275	280	285
Ser Gln Ala Leu Asp Leu Leu Glu Gln Met Leu Ala Phe Asp Pro Gln		
290	295	300
Lys Arg Ile Thr Val Asp Glu Ala Leu Glu His Pro Tyr Leu Ser Ile		
305	310	315 320
Trp His Asp Pro Ala Asp Glu Pro Val Cys Ser Glu Lys Phe Glu Phe		
325	330	335
Ser Phe Glu Ser Val Asn Asp Met Glu Asp Leu Lys Gln Met Val Ile		
340	345	350
Gln Glu Val Gln Asp Phe Arg Leu Phe Val Arg Gln Pro Leu Leu Glu		
355	360	365
Glu Gln Arg Gln Leu Gln Leu Gln Gln Gln Gln Gln Gln Gln		

370 375 380
 Gln Gln Gln Gln Gln Gln Gln Pro Ser Asp Val Asp Asn Gly Asn Ala
 385 390 395 400
 Ala Ala Ser Glu Glu Asn Tyr Pro Lys Gln Met Ala Thr Ser Asn Ser
 405 410 415
 Val Ala Pro Gln Gln Glu Ser Phe Gly Ile His Ser Gln Asn Leu Pro
 420 425 430
 Arg His Asp Ala Asp Phe Pro Pro Arg Pro Gln Glu Ser Met Met Glu
 435 440 445
 Met Arg Pro Ala Thr Gly Asn Thr Ala Asp Ile Pro Pro Gln Asn Asp
 450 455 460
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 Arg Lys Tyr Phe

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<211> 3302

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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 ctaatttcca atgttattta gttttaagca tatctttgtt tctaacagga aactcaggcc 180
 cacatccgca aaaaaatatg tgccaaaaaa ctttcaacac ttcaaagata cttaccactg 240
 caggaaaata atctacgtgt aacggtttga aaataaattt gacttcataa ttggacataa 300
 gtactccatc gccatccctt tttaaagaag tttccacaag aatgaatggc taatcgcaac 360
 taaatctttt ccttgcaaac gtaacacagt atcgacattt tcttactcaa tccaacgaag 420

31

105	110	115	
att ata agg tcc gaa caa cgc ctg gaa gac gca cac ttt caa agc ttc			1399
Ile Ile Arg Ser Glu Gln Arg Leu Glu Asp Ala His Phe Gln Ser Phe			
120	125	130	
ata tat cag ata ctg tgt gct ctg aaa tac ata cat tct gct aat gtt			1447
Ile Tyr Gln Ile Leu Cys Ala Leu Lys Tyr Ile His Ser Ala Asn Val			
135	140	145	
tta cat tgt gac ctg aaa cca aaa aac tta ctt gtt aat agt gat tgc			1495
Leu His Cys Asp Leu Lys Pro Lys Asn Leu Leu Val Asn Ser Asp Cys			
150	155	160	165
caa cta aaa att tgt aat ttt ggg cta tcg tgt agt tat tca gaa aac			1543
Gln Leu Lys Ile Cys Asn Phe Gly Leu Ser Cys Ser Tyr Ser Glu Asn			
170	175	180	
cac aag gtt aac gac ggc ttc att aag ggt tat ata acc tcg ata tgg			1591
His Lys Val Asn Asp Gly Phe Ile Lys Gly Tyr Ile Thr Ser Ile Trp			
185	190	195	
tat aaa gca cca gaa att ttg ctg aat tat caa gaa tgc aca aaa gct			1639
Tyr Lys Ala Pro Glu Ile Leu Leu Asn Tyr Gln Glu Cys Thr Lys Ala			
200	205	210	
gtc gat att tgg tca aca ggc tgt atc ttg gcc gaa cta ctt ggt agg			1687
Val Asp Ile Trp Ser Thr Gly Cys Ile Leu Ala Glu Leu Leu Gly Arg			
215	220	225	
aaa cca atg ttt gaa ggg aag gat tat gta gat cat ttg aat cat att			1735
Lys Pro Met Phe Glu Gly Lys Asp Tyr Val Asp His Leu Asn His Ile			
230	235	240	245
cta caa ata ctt gga aca cca cct gag gaa aca ttg cag gaa att gcc			1783
Leu Gln Ile Leu Gly Thr Pro Pro Glu Glu Thr Leu Gln Glu Ile Ala			
250	255	260	
tct caa aag gtg tat aat tat atc ttt cag ttc ggt aat atc ccg gga			1831
Ser Gln Lys Val Tyr Asn Tyr Ile Phe Gln Phe Gly Asn Ile Pro Gly			
265	270	275	
aga tcg ttt gaa agc ata cta cct ggt gct aat cca gaa gcg ctt gaa			1879
Arg Ser Phe Glu Ser Ile Leu Pro Gly Ala Asn Pro Glu Ala Leu Glu			
280	285	290	
ttg cta aag aaa atg cta gaa ttt gat cct aaa aaa agg att act gta			1927
Leu Leu Lys Lys Met Leu Glu Phe Asp Pro Lys Lys Arg Ile Thr Val			

295	300	305	
gag gat gca cta gag cat cca tat ttg tca atg tgg cat gat ata gat			1975
Glu Asp Ala Leu Glu His Pro Tyr Leu Ser Met Trp His Asp Ile Asp			
310	315	320	325
gag gaa ttc tca tgt caa aag acc ttt aga ttc gaa ttc gag cat atc			2023
Glu Glu Phe Ser Cys Gln Lys Thr Phe Arg Phe Glu Phe Glu His Ile			
330	335	340	
gaa agt atg gcg gaa tta gga aac gaa gtt ata aag gaa gta ttt gat			2071
Glu Ser Met Ala Glu Leu Gly Asn Glu Val Ile Lys Glu Val Phe Asp			
345	350	355	
ttc agg aaa gtt gtt aga aaa cat cct att agc ggt gat tcc cca tca			2119
Phe Arg Lys Val Val Arg Lys His Pro Ile Ser Gly Asp Ser Pro Ser			
360	365	370	
tca tca cta tct tta gag gat gcc att cct caa gaa gtt gta cag gtc			2167
Ser Ser Leu Ser Leu Glu Asp Ala Ile Pro Gln Glu Val Val Gln Val			
375	380	385	
cat cct tct agg aaa gtt tta ccc agt tat agt cct gaa ttt tcc tat			2215
His Pro Ser Arg Lys Val Leu Pro Ser Tyr Ser Pro Glu Phe Ser Tyr			
390	395	400	405
gta agc caa ctt cca tca cta act aca acc cag cca tat caa aac ctt			2263
Val Ser Gln Leu Pro Ser Leu Thr Thr Gln Pro Tyr Gln Asn Leu			
410	415	420	
atg gga ata agc tct aat tca ttt cag ggt gtt aac taaaaggaaa			2309
Met Gly Ile Ser Ser Asn Ser Phe Gln Gly Val Asn			
425	430		
acaccttcaa acaagatact aagcatgaaa atagtgaact actgaacgga cctactgagc			2369
caaatataac aaaaatgagc ccagtttcat cgtctcccc aggtcacgat ataaatgtca			2429
atgatggtac aaacaaaaat acaaatgagg atgacagcga ttttttcttc gacctagaaa			2489
aagaacttga attattttaga cgataaattt ttgtagcaga aaaccacaac taatagatgc			2549
gcacatacac tatctataat gaatatgtaa aatgcctgtt caccttctta attattggta			2609
tatacttcaa atattgcaaa aagagaaagt cctctcggcg gttttgcagt tccttccgaa			2669
agcgggaaaa accaaaatgt gagaaagtag gatacaccat tgcgtagatt cgcgatgatc			2729

cgaatataaa catgattccc tcgtcagtc tctctcaagt tttctttccc gttttaaata 2789
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 atgttccaga aaataaaata tttcatggta cct 3302

<210> 14

<211> 433

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

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Phe	Ile	Leu	Asn	Lys	His	Phe	His	Leu	Thr	Gly	Lys	Ile	Gly	Arg	Gly
			20					25						30	
Ser	His	Ser	Leu	Ile	Cys	Ser	Ser	Thr	Tyr	Thr	Glu	Ser	Asn	Glu	Glu
		35						40					45		
Thr	His	Val	Ala	Ile	Arg	Lys	Ile	Pro	Asn	Ala	Phe	Gly	Asn	Lys	Leu
		50					55						60		
Ser	Cys	Lys	Arg	Thr	Leu	Arg	Glu	Leu	Lys	Leu	Leu	Arg	His	Leu	Arg
	65					70				75					80
Gly	His	Pro	Asn	Ile	Val	Trp	Leu	Phe	Asp	Thr	Asp	Ile	Val	Phe	Tyr
			85						90					95	
Pro	Asn	Gly	Ala	Leu	Asn	Gly	Val	Tyr	Leu	Tyr	Glu	Glu	Leu	Met	Glu
				100					105					110	

Cys Asp Leu Ser Gln Ile Ile Arg Ser Glu Gln Arg Leu Glu Asp Ala
115 120 125

His Phe Gln Ser Phe Ile Tyr Gln Ile Leu Cys Ala Leu Lys Tyr Ile
130 135 140

His Ser Ala Asn Val Leu His Cys Asp Leu Lys Pro Lys Asn Leu Leu
145 150 155 160

Val Asn Ser Asp Cys Gln Leu Lys Ile Cys Asn Phe Gly Leu Ser Cys
165 170 175

Ser Tyr Ser Glu Asn His Lys Val Asn Asp Gly Phe Ile Lys Gly Tyr
180 185 190

Ile Thr Ser Ile Trp Tyr Lys Ala Pro Glu Ile Leu Leu Asn Tyr Gln
195 200 205

Glu Cys Thr Lys Ala Val Asp Ile Trp Ser Thr Gly Cys Ile Leu Ala
210 215 220

Glu Leu Leu Gly Arg Lys Pro Met Phe Glu Gly Lys Asp Tyr Val Asp
225 230 235 240

His Leu Asn His Ile Leu Gln Ile Leu Gly Thr Pro Pro Glu Glu Thr
245 250 255

Leu Gln Glu Ile Ala Ser Gln Lys Val Tyr Asn Tyr Ile Phe Gln Phe
260 265 270

Gly Asn Ile Pro Gly Arg Ser Phe Glu Ser Ile Leu Pro Gly Ala Asn
275 280 285

Pro Glu Ala Leu Glu Leu Leu Lys Lys Met Leu Glu Phe Asp Pro Lys
290 295 300

Lys Arg Ile Thr Val Glu Asp Ala Leu Glu His Pro Tyr Leu Ser Met
305 310 315 320

Trp His Asp Ile Asp Glu Glu Phe Ser Cys Gln Lys Thr Phe Arg Phe
325 330 335

Glu Phe Glu His Ile Glu Ser Met Ala Glu Leu Gly Asn Glu Val Ile
340 345 350

Lys Glu Val Phe Asp Phe Arg Lys Val Val Arg Lys His Pro Ile Ser
355 360 365

Gly Asp Ser Pro Ser Ser Ser Leu Ser Leu Glu Asp Ala Ile Pro Gln
 370 375 380

Glu Val Val Gln Val His Pro Ser Arg Lys Val Leu Pro Ser Tyr Ser
 385 390 395 400

Pro Glu Phe Ser Tyr Val Ser Gln Leu Pro Ser Leu Thr Thr Thr Gln
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<213> *Saccharomyces cerevisiae*

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<400> 15

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gatacactgt tatgctaaga gacggtgcga tattctgtac gaaaattatt taactattaa 240

ctaaatgtat accacttcac gtgccaccga gtaggtttct aaaatgtgca accatttttag 300

gatatgtgcgc agctctttat tctaaacggg agtcactaca ttactattat cgtgtttttg 360

cccatgtact ttcttataat cttaagacaa caacgggatg ataggcgcat tcggactttc 420

attgatgcaa atgtgtgaaa aatgcatcca aaagacaact tttgtacaga atacaattgc 480

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ttcggaaccg agcaaccatt tccgaatgta gtagtagttg aaggagtaaa tcgaccttat 600

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37

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Ser Gln Ile Thr Asp Gly Gln Val Gln Ala Ala Lys Ser Thr Ala Ala			
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gct gcc tct cag att tct gac ggc caa gtt cag gcc act acc tct act			1543
Ala Ala Ser Gln Ile Ser Asp Gly Gln Val Gln Ala Thr Thr Ser Thr			
	170	175	180
aag gct gct gca tcc caa att aca gat ggg cag ata caa gca tct aaa			1591
Lys Ala Ala Ala Ser Gln Ile Thr Asp Gly Gln Ile Gln Ala Ser Lys			
	185	190	195
act acc agt ggc gct agt caa gta agt gat ggc caa gtc cag gct act			1639
Thr Thr Ser Gly Ala Ser Gln Val Ser Asp Gly Gln Val Gln Ala Thr			
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gct gaa gtg aaa gac gct aac gat cca gtc gat gtt gtt tcc tgt aat			1687
Ala Glu Val Lys Asp Ala Asn Asp Pro Val Asp Val Val Ser Cys Asn			
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Asn Asn Ser Thr Leu Ser Met Ser Leu Ser Lys Gly Ile Leu Thr Asp			
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agg aag ggt aga att ggc tct atc gtt gcc aac aga cag ttc caa ttc			1783
Arg Lys Gly Arg Ile Gly Ser Ile Val Ala Asn Arg Gln Phe Gln Phe			
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Asp Gly Pro Pro Pro Gln Ala Gly Ala Ile Tyr Ala Ala Gly Trp Ser			
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atc acc cca gaa ggt aac tta gct ctt ggt gac cag gat act ttt tac			1879
Ile Thr Pro Glu Gly Asn Leu Ala Leu Gly Asp Gln Asp Thr Phe Tyr			
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caa tgt ttg tct ggt gac ttc tat aac ttg tat gat aag cac att ggt			1927
Gln Cys Leu Ser Gly Asp Phe Tyr Asn Leu Tyr Asp Lys His Ile Gly			
	295	300	305
tct cag tgc cat gaa gtt tat ttg caa gct ata gat tta att gac tgt			1975
Ser Gln Cys His Glu Val Tyr Leu Gln Ala Ile Asp Leu Ile Asp Cys			
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Leu Ala Ala Tyr Ala Pro Lys Asp Pro Trp Ser Thr Leu Thr Pro Ser

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25

30

Ala Thr Tyr Lys Gly Gly Ile Thr Asp Tyr Ser Ser Ser Phe Gly Ile

35

40

45

Ala Ile Glu Ala Val Ala Thr Ser Ala Ser Ser Val Ala Ser Ser Lys
50 55 60

Ala Lys Arg Ala Ala Ser Gln Ile Gly Asp Gly Gln Val Gln Ala Ala
65 70 75 80

Thr Thr Thr Ala Ala Val Ser Lys Lys Ser Thr Ala Ala Ala Val Ser
85 90 95

Gln Ile Thr Asp Gly Gln Val Gln Ala Ala Lys Ser Thr Ala Ala Ala
100 105 110

Val Ser Gln Ile Thr Asp Gly Gln Val Gln Ala Ala Lys Ser Thr Ala
115 120 125

Ala Ala Val Ser Gln Ile Thr Asp Gly Gln Val Gln Ala Ala Lys Ser
130 135 140

Thr Ala Ala Ala Val Ser Gln Ile Thr Asp Gly Gln Val Gln Ala Ala
145 150 155 160

Lys Ser Thr Ala Ala Ala Ala Ser Gln Ile Ser Asp Gly Gln Val Gln
165 170 175

Ala Thr Thr Ser Thr Lys Ala Ala Ala Ser Gln Ile Thr Asp Gly Gln
180 185 190

Ile Gln Ala Ser Lys Thr Thr Ser Gly Ala Ser Gln Val Ser Asp Gly
195 200 205

Gln Val Gln Ala Thr Ala Glu Val Lys Asp Ala Asn Asp Pro Val Asp
210 215 220

Val Val Ser Cys Asn Asn Asn Ser Thr Leu Ser Met Ser Leu Ser Lys
225 230 235 240

Gly Ile Leu Thr Asp Arg Lys Gly Arg Ile Gly Ser Ile Val Ala Asn
245 250 255

Arg Gln Phe Gln Phe Asp Gly Pro Pro Pro Gln Ala Gly Ala Ile Tyr
260 265 270

Ala Ala Gly Trp Ser Ile Thr Pro Glu Gly Asn Leu Ala Leu Gly Asp
275 280 285

Gln Asp Thr Phe Tyr Gln Cys Leu Ser Gly Asp Phe Tyr Asn Leu Tyr
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 305 310 315 320

Asp Leu Ile Asp Cys
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 tctgggcaaa gtacggccgt actttcttca ctcggtatga ttttgaaaaa gttgaaacag 180
 aaaaagctaa caagattgtc gatcaattga gagcatatgt taccaaatac ggtgttggtta 240
 attccgcctt ccagccgat gagtctctta aggtcaccga ttgtggtgat tttcataca 300
 cagatttga cggttctgtt tctgaccatc aaggtttata tgtcaagctt tccaatggtg 360
 caagattcgt tctaagattg tcaggtaacg gttcttcagg tgctaccatt agattgtaca 420
 ttgaaaaata ctgcgatgat aaatcacaat accaaaagac agctgaagaa tacttgaagc 480
 caattattaa ctcggtcatc aagttcttga actttaaaca agtttttagga actgaagaac 540
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 atgaatatta acggtaaaga agaaaatttc aattttttga acacatactt tatatactta 660
 atagatccat atttcgacat attagcaaac gattgcatag gtttctgagt cttttttttt 720
 tttttttcat aaggaggaga atatttttgt taatcgcagt atcttcttca taagtgtgt 780
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 cctacccga gttttttatt atatttcctt cgagaaatct gtaaatggc cgtcatcctt 900
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ata	tcc	aag	ttt	aag	tta	gga	agg	tcc	aaa	gaa	gat	gat	ggg	agt	agt	1063
Ile	Ser	Lys	Phe	Lys	Leu	Gly	Arg	Ser	Lys	Glu	Asp	Asp	Gly	Ser	Ser	
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gaa	gat	gaa	aat	gaa	aaa	tcg	tgg	ggt	aat	ggc	ctg	ttt	cat	ttc	cac	1111
Glu	Asp	Glu	Asn	Glu	Lys	Ser	Trp	Gly	Asn	Gly	Leu	Phe	His	Phe	His	
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cat	gga	gaa	aaa	cat	cac	gat	ggt	agc	ccg	aag	aat	cat	aat	cat	gaa	1159
His	Gly	Glu	Lys	His	His	Asp	Gly	Ser	Pro	Lys	Asn	His	Asn	His	Glu	
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cac	gaa	cac	cat	ata	aga	aag	atc	aat	aca	aat	gag	act	ctc	cca	agt	1207
His	Glu	His	His	Ile	Arg	Lys	Ile	Asn	Thr	Asn	Glu	Thr	Leu	Pro	Ser	
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tcc	tta	agt	tct	cca	aaa	tta	cgt	aat	gat	gca	tcc	ttc	aag	aat	cca	1255
Ser	Leu	Ser	Ser	Pro	Lys	Leu	Arg	Asn	Asp	Ala	Ser	Phe	Lys	Asn	Pro	
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tcg	ggg	ata	gga	aat	gac	aat	tct	aag	gct	tcc	gaa	agg	aaa	gct	agt	1303
Ser	Gly	Ile	Gly	Asn	Asp	Asn	Ser	Lys	Ala	Ser	Glu	Arg	Lys	Ala	Ser	
				90				95					100			
cag	tcg	tct	act	gag	acg	cag	gga	ccg	agt	tcg	gaa	tcc	gga	cta	atg	1351
Gln	Ser	Ser	Thr	Glu	Thr	Gln	Gly	Pro	Ser	Ser	Glu	Ser	Gly	Leu	Met	
				105				110					115			
aca	gtg	aag	gtg	tat	tct	ggt	aaa	gat	ttt	act	ctt	ccc	ttc	cct	atc	1399
Thr	Val	Lys	Val	Tyr	Ser	Gly	Lys	Asp	Phe	Thr	Leu	Pro	Phe	Pro	Ile	
				120				125					130			
acc	tct	aac	tct	act	att	tta	caa	aaa	cta	cta	agt	tcc	ggc	atc	ctt	1447
Thr	Ser	Asn	Ser	Thr	Ile	Leu	Gln	Lys	Leu	Leu	Ser	Ser	Gly	Ile	Leu	
				135				140					145			
act	tca	tca	tcc	aat	gac	gct	tcc	gaa	gtt	gca	gcc	ata	atg	cgg	cag	1495
Thr	Ser	Ser	Ser	Asn	Asp	Ala	Ser	Glu	Val	Ala	Ala	Ile	Met	Arg	Gln	
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cta	cca	cga	tac	aag	aga	gtg	gat	caa	gat	tca	gca	ggg	gaa	ggc	ttg	1543
Leu	Pro	Arg	Tyr	Lys	Arg	Val	Asp	Gln	Asp	Ser	Ala	Gly	Glu	Gly	Leu	
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 Ile Asp Arg Ala Phe Ala Thr Lys Phe Ile Pro Ser Ser Ile Leu Leu
 185 190 195

cct ggg tca aca aat tca agc cca tta ctt tat ttt aca att gaa ttt 1639
 Pro Gly Ser Thr Asn Ser Ser Pro Leu Leu Tyr Phe Thr Ile Glu Phe
 200 205 210

gat aat tct att act act att agt cca gat atg gga acg atg gag caa 1687
 Asp Asn Ser Ile Thr Thr Ile Ser Pro Asp Met Gly Thr Met Glu Gln
 215 220 225

cca gtg ttt aac aaa ata tcg aca ttt gat gta aca aga aaa tta cga 1735
 Pro Val Phe Asn Lys Ile Ser Thr Phe Asp Val Thr Arg Lys Leu Arg
 230 235 240 245

ttt tta aaa atc gat gtc ttt gca agg att cca tcc cta ctt tta ccc 1783
 Phe Leu Lys Ile Asp Val Phe Ala Arg Ile Pro Ser Leu Leu Leu Pro
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tct aaa aac tgg caa cag gag att ggc gag cag gac gaa gta ctg aag 1831
 Ser Lys Asn Trp Gln Gln Glu Ile Gly Glu Gln Asp Glu Val Leu Lys
 265 270 275

gag att tta aaa aaa atc aat aca aat cag gat atc cat ttg gac tcc 1879
 Glu Ile Leu Lys Lys Ile Asn Thr Asn Gln Asp Ile His Leu Asp Ser
 280 285 290

ttc cat tta cct ttg aat tta aaa atc gat tct gca gcc caa ata aga 1927
 Phe His Leu Pro Leu Asn Leu Lys Ile Asp Ser Ala Ala Gln Ile Arg
 295 300 305

cta tac aat cac cat tgg att tct tta gaa agg gga tat ggt aaa tta 1975
 Leu Tyr Asn His His Trp Ile Ser Leu Glu Arg Gly Tyr Gly Lys Leu
 310 315 320 325

aat atc acg gtg gac tac aaa cct tct aag aac aag cct ctc tcc att 2023
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 330 335 340

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 Asp Asp Phe Asp Leu Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys
 345 350 355

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 360 365 370

gct ctg aga aaa gca tat att gta tcg aaa tgt gaa gtg aca cat act 2167
 Ala Leu Arg Lys Ala Tyr Ile Val Ser Lys Cys Glu Val Thr His Thr
 375 380 385

tta gcg gag agg act gtc cta gca aga gtt gac tgc ccc ttt att gtt 2215
 Leu Ala Glu Arg Thr Val Leu Ala Arg Val Asp Cys Pro Phe Ile Val
 390 395 400 405

ccg ttg aag ttc tca ttc caa tct ccg gag aag ttg tac cta gta tta 2263
 Pro Leu Lys Phe Ser Phe Gln Ser Pro Glu Lys Leu Tyr Leu Val Leu
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gct ttc att aat ggc ggt gaa ctg ttc tac cat tta caa cac gag gga 2311
 Ala Phe Ile Asn Gly Gly Glu Leu Phe Tyr His Leu Gln His Glu Gly
 425 430 435

cga ttc agt cta gca cgc tcc cgt ttt tat att gca gaa cta tta tgt 2359
 Arg Phe Ser Leu Ala Arg Ser Arg Phe Tyr Ile Ala Glu Leu Leu Cys
 440 445 450

gct ctc gat tca tta cac aaa ctt gac gtc att tat cgt gac cta aag 2407
 Ala Leu Asp Ser Leu His Lys Leu Asp Val Ile Tyr Arg Asp Leu Lys
 455 460 465

cct gaa aac att cta ttg gat tac caa gga cat att gca ctg tgt gat 2455
 Pro Glu Asn Ile Leu Leu Asp Tyr Gln Gly His Ile Ala Leu Cys Asp
 470 475 480 485

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 Phe Gly Leu Cys Lys Leu Asn Met Lys Asp Asn Asp Lys Thr Asp Thr
 490 495 500

ttc tgt ggt act ccc gaa tat ttg gca cca gaa atc ttg ttg ggg cag 2551
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ggc tat act aaa aca gtt gac tgg tgg aca tta ggt atc tta ctg tat 2599
 Gly Tyr Thr Lys Thr Val Asp Trp Trp Thr Leu Gly Ile Leu Leu Tyr
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 Glu Met Met Thr Gly Leu Pro Pro Tyr Tyr Asp Glu Asn Val Pro Val
 535 540 545

atg tac aag aaa att ctg cag caa ccg cta cta ttt cct gat gga ttt 2695
 Met Tyr Lys Lys Ile Leu Gln Gln Pro Leu Leu Phe Pro Asp Gly Phe
 550 555 560 565

gac cct gcg gca aaa gac cta tta att ggc ctc tta agc aga gac cca 2743
 Asp Pro Ala Ala Lys Asp Leu Leu Ile Gly Leu Leu Ser Arg Asp Pro
 570 575 580

agc aga aga ctc ggc gtt aac ggt aca gat gaa att cgt aac cat cct 2791
 Ser Arg Arg Leu Gly Val Asn Gly Thr Asp Glu Ile Arg Asn His Pro
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 Pro Pro Tyr Lys Pro Ile Val Lys Ser Glu Ile Asp Thr Ala Asn Phe
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 Asp Gln Glu Phe Thr Lys Glu Lys Pro Ile Asp Ser Val Val Asp Glu
 630 635 640 645

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 Tyr Leu Ser Ala Ser Ile Gln Lys Gln Phe Gly Gly Trp Thr Tyr Ile
 650 655 660

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<213> *Saccharomyces cerevisiae*

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30

Leu Phe His Phe His His Gly Glu Lys His His Asp Gly Ser Pro Lys

35

40

45

Asn His Asn His Glu His Glu His His Ile Arg Lys Ile Asn Thr Asn

50

55

60

Glu Thr Leu Pro Ser Ser Leu Ser Ser Pro Lys Leu Arg Asn Asp Ala

65

70

75

80

Ser Phe Lys Asn Pro Ser Gly Ile Gly Asn Asp Asn Ser Lys Ala Ser

85

90

95

Glu Arg Lys Ala Ser Gln Ser Ser Thr Glu Thr Gln Gly Pro Ser Ser

100

105

110

Glu Ser Gly Leu Met Thr Val Lys Val Tyr Ser Gly Lys Asp Phe Thr

115

120

125

Leu Pro Phe Pro Ile Thr Ser Asn Ser Thr Ile Leu Gln Lys Leu Leu

130

135

140

Ser Ser Gly Ile Leu Thr Ser Ser Ser Asn Asp Ala Ser Glu Val Ala
 145 150 155 160

Ala Ile Met Arg Gln Leu Pro Arg Tyr Lys Arg Val Asp Gln Asp Ser
 165 170 175

Ala Gly Glu Gly Leu Ile Asp Arg Ala Phe Ala Thr Lys Phe Ile Pro
 180 185 190

Ser Ser Ile Leu Leu Pro Gly Ser Thr Asn Ser Ser Pro Leu Leu Tyr
 195 200 205

Phe Thr Ile Glu Phe Asp Asn Ser Ile Thr Thr Ile Ser Pro Asp Met
 210 215 220

Gly Thr Met Glu Gln Pro Val Phe Asn Lys Ile Ser Thr Phe Asp Val
 225 230 235 240

Thr Arg Lys Leu Arg Phe Leu Lys Ile Asp Val Phe Ala Arg Ile Pro
 245 250 255

Ser Leu Leu Leu Pro Ser Lys Asn Trp Gln Gln Glu Ile Gly Glu Gln
 260 265 270

Asp Glu Val Leu Lys Glu Ile Leu Lys Lys Ile Asn Thr Asn Gln Asp
 275 280 285

Ile His Leu Asp Ser Phe His Leu Pro Leu Asn Leu Lys Ile Asp Ser
 290 295 300

Ala Ala Gln Ile Arg Leu Tyr Asn His His Trp Ile Ser Leu Glu Arg
 305 310 315 320

Gly Tyr Gly Lys Leu Asn Ile Thr Val Asp Tyr Lys Pro Ser Lys Asn
 325 330 335

Lys Pro Leu Ser Ile Asp Asp Phe Asp Leu Leu Lys Val Ile Gly Lys
 340 345 350

Gly Ser Phe Gly Lys Val Met Gln Val Arg Lys Lys Asp Thr Gln Lys
 355 360 365

Ile Tyr Ala Leu Lys Ala Leu Arg Lys Ala Tyr Ile Val Ser Lys Cys
 370 375 380

Glu Val Thr His Thr Leu Ala Glu Arg Thr Val Leu Ala Arg Val Asp
 385 390 395 400

Cys Pro Phe Ile Val Pro Leu Lys Phe Ser Phe Gln Ser Pro Glu Lys
 405 410 415

Leu Tyr Leu Val Leu Ala Phe Ile Asn Gly Gly Glu Leu Phe Tyr His
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Leu Gln His Glu Gly Arg Phe Ser Leu Ala Arg Ser Arg Phe Tyr Ile
 435 440 445

Ala Glu Leu Leu Cys Ala Leu Asp Ser Leu His Lys Leu Asp Val Ile
 450 455 460

Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Tyr Gln Gly His
 465 470 475 480

Ile Ala Leu Cys Asp Phe Gly Leu Cys Lys Leu Asn Met Lys Asp Asn
 485 490 495

Asp Lys Thr Asp Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu
 500 505 510

Ile Leu Leu Gly Gln Gly Tyr Thr Lys Thr Val Asp Trp Trp Thr Leu
 515 520 525

Gly Ile Leu Leu Tyr Glu Met Met Thr Gly Leu Pro Pro Tyr Tyr Asp
 530 535 540

Glu Asn Val Pro Val Met Tyr Lys Lys Ile Leu Gln Gln Pro Leu Leu
 545 550 555 560

Phe Pro Asp Gly Phe Asp Pro Ala Ala Lys Asp Leu Leu Ile Gly Leu
 565 570 575

Leu Ser Arg Asp Pro Ser Arg Arg Leu Gly Val Asn Gly Thr Asp Glu
 580 585 590

Ile Arg Asn His Pro Phe Phe Lys Asp Ile Ser Trp Lys Lys Leu Leu
 595 600 605

Leu Lys Gly Tyr Ile Pro Pro Tyr Lys Pro Ile Val Lys Ser Glu Ile
 610 615 620

Asp Thr Ala Asn Phe Asp Gln Glu Phe Thr Lys Glu Lys Pro Ile Asp
 625 630 635 640

Ser Val Val Asp Glu Tyr Leu Ser Ala Ser Ile Gln Lys Gln Phe Gly
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Gly Arg Ser Ile Ser
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<211> 2765

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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<222> (1001)..(1762)

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 actaattcaa attttcacaa aagaagaatt cgaacataat ttcattggtg aagaatcggt 180
 accattggat aaacaagtaa ttttctcata tgtagtcgaa cagcccgatg gaaaaattac 240
 agacttcttc tcattttact cattgccatt cacaatccta aataacacaa aatataagga 300
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 atttaattat agagcaaagc cgattaccgg tggcttgaat cccgacaata gtaacgacat 600
 taaaaggcgt agcaatgtcg gtgttggttat gttgtagtgg ctgaaaggac gaggcgtata 660
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 tgacgaagtg aaaaaataat taatccaatg gctggcttta gagtgtcagc ctccaaaata 780
 aatccaaaaa tagacaaaga gaatcactat aattaccgcc ttggagtcca agttggcttg 840
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50

170	175	180	
tcc tca tca aaa ccg gaa tca agc acc aag gta gta agc act atc aaa			1591
Ser Ser Ser Lys Pro Glu Ser Ser Thr Lys Val Val Ser Thr Ile Lys			
185	190	195	
tca act tat acc act acg tca ggt tct aca gta gag aca ctg acc act			1639
Ser Thr Tyr Thr Thr Thr Ser Gly Ser Thr Val Glu Thr Leu Thr Thr			
200	205	210	
aca tac aag tct aca gtc aac ggt aag gta gcg tcc gta atg tcc aat			1687
Thr Tyr Lys Ser Thr Val Asn Gly Lys Val Ala Ser Val Met Ser Asn			
215	220	225	
tct acc aat ggc gcc ttt gcc ggc act cac ata gct tat ggt gcg ggt			1735
Ser Thr Asn Gly Ala Phe Ala Gly Thr His Ile Ala Tyr Gly Ala Gly			
230	235	240	245
gca ttc gcc gtt ggt gcc ctt ttg tta tagaatgtat aatcagttct			1782
Ala Phe Ala Val Gly Ala Leu Leu Leu			
250			
gtataccacc acatagttct gcattttaat aaaactcttt ctttttatac actgtaggta			1842
accaataata taactattgt tatcatcgtg cttgcgtatt ttttttcttt cgggtgaaaa			1902
actccgcagt atttctcgt ctccttgat aataagctag aaaaaaaaaa tatatatgac			1962
agatggatga gtaatcatat tcaataagta ttgtctggct tctgagacgg cggtagata			2022
tccttaagag ttgcaatggc ctttttacac aaaagcacac atatatttcc taccgatttt			2082
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agtgtacaaa gtagtacgat agcagacagc cgggtgaagt tttcaagtgg cttcaatatg			2442
ggtatcaaat ctaaggtaga ggattggctg cgactaaat ttgacgaaaa cgtaagaaa			2502
agcagaatgg gcatggcatt tgttatccaa aaactcgaag aggcgagaaa tcctcagttt			2562

tgatgttccc atttaaagat ctttaaagat atcaccatgg gcgagcgaaa ttgagaaaac 2622
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<211> 254

<212> PRT

<213> *Saccharomyces cerevisiae*

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20 25 30

Ser Gln Lys Glu Ser Ser Asn Ser Gln Glu Ile Thr Pro Thr Thr Thr

35 40 45

Lys Glu Ala Gln Glu Ser Ala Ser Thr Val Val Ser Thr Gly Lys Ser

50 55 60

Leu Val Gln Thr Ser Asn Val Val Ser Asn Thr Tyr Ala Val Ala Pro

65 70 75 80

Ser Thr Thr Val Val Thr Thr Asp Ala Gln Gly Lys Thr Thr Thr Gln

85 90 95

Tyr Leu Trp Trp Val Ala Glu Ser Asn Ser Ala Val Ser Thr Thr Ser

100 105 110

Thr Ala Ser Val Gln Pro Thr Gly Glu Thr Ser Ser Gly Ile Thr Asn

115 120 125

Ser Ala Ser Ser Ser Thr Thr Ser Thr Ser Thr Asp Gly Pro Val Thr

130 135 140

Ile Val Thr Thr Thr Asn Ser Leu Gly Glu Thr Tyr Thr Ser Thr Val

145 150 155 160

Trp Trp Leu Pro Ser Ser Ala Thr Thr Asp Asn Thr Ala Ser Ser Ser

165 170 175

Lys Ser Ser Ser Gly Ser Ser Ser Lys Pro Glu Ser Ser Thr Lys Val
 180 185 190

Val Ser Thr Ile Lys Ser Thr Tyr Thr Thr Thr Ser Gly Ser Thr Val
 195 200 205

Glu Thr Leu Thr Thr Thr Tyr Lys Ser Thr Val Asn Gly Lys Val Ala
 210 215 220

Ser Val Met Ser Asn Ser Thr Asn Gly Ala Phe Ala Gly Thr His Ile
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Ala Tyr Gly Ala Gly Ala Phe Ala Val Gly Ala Leu Leu Leu
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<210> 21

<211> 3335

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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<222> (1001) .. (2332)

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agggacggac aaacacaaga cgatgctgca cgtgggttagt tttgtaagcg cagggttacga 180

taaagagcat aaacaaatca ttactaagag cggtatacaa gaataaagtg acaaacagtt 240

ctccctatctt aacgcactta acgtagggttc catcattatg atgctattgc cacatcaaatt 300

ctccttttga ctgaaccgcg attagtaatt gcccgctttt cttttcttcc gcggttgggc 360

cccataaata gaaaaaaaaa gaaagaaagc gtttaaataa atagagttag cggattttcta 420

ttatctgaaa accgggttat aatgcacgtg atatgcacgt gggagctggg cggctatctt 480

tttctttttc aaatgtatct gagtcgttta aaatagcact cccggttgac ccgccaactc 540

atctttgttt tctcttttac gaaaaggctt taaattaagg cccgcatttt cgggtatcctt 600

gagggaaaaa aaccaaagaa acccaaaaaa gaccacaaag ctgggatatc ttaattagta 660

54

135	140	145	
act tcg tta caa tct gtc gat gga ttc tca gcc ttg aaa aaa gtt aac			1495
Thr Ser Leu Gln Ser Val Asp Gly Phe Ser Ala Leu Lys Lys Val Asn			
150	155	160	165
gtg ttc aac gtc aat aac aat aag aaa tta acc tcg atc aaa tct cca			1543
Val Phe Asn Val Asn Asn Asn Lys Lys Thr Ser Ile Lys Ser Pro			
170	175		180
gtt gaa aca gtc agc gat tct tta caa ttt tcg ttc aac ggt aac cag			1591
Val Glu Thr Val Ser Asp Ser Leu Gln Phe Ser Phe Asn Gly Asn Gln			
185	190		195
act aaa atc acc ttc gat gac ttg gtt tgg gca aac aat atc agt ttg			1639
Thr Lys Ile Thr Phe Asp Asp Leu Val Trp Ala Asn Asn Ile Ser Leu			
200	205		210
acc gat gtc cac tct gtt tcc ttc gct aac ttg caa aag att aac tct			1687
Thr Asp Val His Ser Val Ser Phe Ala Asn Leu Gln Lys Ile Asn Ser			
215	220		225
tca ttg ggt ttc atc aac aac tcc atc tca agt ttg aat ttc act aag			1735
Ser Leu Gly Phe Ile Asn Asn Ser Ile Ser Ser Leu Asn Phe Thr Lys			
230	235	240	245
cta aac acc att ggc caa acc ttc agt atc gtt tcc aat gac tac ttg			1783.
Leu Asn Thr Ile Gly Gln Thr Phe Ser Ile Val Ser Asn Asp Tyr Leu			
250	255		260
aag aac ttg tcg ttc tct aat ttg tca acc ata ggt ggt gct ctt gtc			1831
Lys Asn Leu Ser Phe Ser Asn Leu Ser Thr Ile Gly Gly Ala Leu Val			
265	270		275
gtt gct aac aac act ggt tta caa aaa att ggt ggt ctc gac aac cta			1879
Val Ala Asn Asn Thr Gly Leu Gln Lys Ile Gly Gly Leu Asp Asn Leu			
280	285		290
aca acc att ggc ggt act ttg gaa gtt gtt ggt aac ttc acc tcc ttg			1927
Thr Thr Ile Gly Gly Thr Leu Glu Val Val Gly Asn Phe Thr Ser Leu			
295	300		305
aac cta gac tct ttg aag tct gtc aag ggt ggc gca gat gtc gaa tca			1975
Asn Leu Asp Ser Leu Lys Ser Val Lys Gly Gly Ala Asp Val Glu Ser			
310	315	320	325
aag tca agc aat ttc tcc tgt aat gct ttg aaa gct ttg caa aag aaa			2023
Lys Ser Ser Asn Phe Ser Cys Asn Ala Leu Lys Ala Leu Gln Lys Lys			

330	335	340	
ggg ggt atc aag ggt gaa tct ttt gtc tgc aaa aat ggt gca tca tcc			2071
Gly Gly Ile Lys Gly Glu Ser Phe Val Cys Lys Asn Gly Ala Ser Ser			
345	350	355	
aca tct gtt aaa cta tcg tcc act tcc aaa tct caa tca agc caa act			2119
Thr Ser Val Lys Leu Ser Ser Thr Ser Lys Ser Gln Ser Ser Gln Thr			
360	365	370	
act gcc aag gtt tcc aag tca tct tct aag gcc gag gaa aag aag ttc			2167
Thr Ala Lys Val Ser Lys Ser Ser Ser Lys Ala Glu Glu Lys Lys Phe			
375	380	385	
act tct ggc gat atc aag gct gct gct tct gcc tct agt gtt tct agt			2215
Thr Ser Gly Asp Ile Lys Ala Ala Ala Ser Ala Ser Ser Val Ser Ser			
390	395	400	405
tct ggc gct tcc agc tct agc tct aag agt tcc aaa ggc aat gcc gct			2263
Ser Gly Ala Ser Ser Ser Ser Lys Ser Ser Lys Gly Asn Ala Ala			
410	415	420	
atc atg gca cca att ggc caa aca acc cct ttg gtc ggt ctt ttg acg			2311
Ile Met Ala Pro Ile Gly Gln Thr Thr Pro Leu Val Gly Leu Leu Thr			
425	430	435	
gca atc atc atg tct ata atg taatggaatg aagaaatatt cttcattttt			2362
Ala Ile Ile Met Ser Ile Met			
440			
gataactagt acctgtcatt cactgacatgt gaacaaataa aaacatttat ttaaaaattt 2422			
tatgtattca aatatttttcg ggaaagagat aaaagtaacg acacttaaaa atttaaaaaa 2482			
tcacaatact ttattttactc agtcttttga tcagctccgg cacctccttg ttgttgcttc 2542			
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tcaatctggg cattcaaaca gtattctcca gaaacttcaa catcctgtat attaacgggt 2962
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<211> 444

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 22

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 20 25 30

Ile Ser Ser His Ala Thr Ala Thr Ala Gln Ser Asp Leu Asp Lys Tyr
 35 40 45

Ser Arg Cys Asp Thr Leu Val Gly Asn Leu Thr Ile Gly Gly Gly Leu
 50 55 60

Lys Thr Gly Ala Leu Ala Asn Val Lys Glu Ile Asn Gly Ser-Leu Thr
 65 70 75 80

Ile Phe Asn Ala Thr Asn Leu Thr Ser Phe Ala Ala Asp Ser Leu Glu
 85 90 95

Ser Ile Thr Asp Ser Leu Asn Leu Gln Ser Leu Thr Ile Leu Thr Ser
 100 105 110

Ala Ser Phe Gly Ser Leu Gln Ser Val Asp Ser Ile Lys Leu Ile Thr
 115 120 125

Leu Pro Ala Ile Ser Ser Phe Thr Ser Asn Ile Lys Ser Ala Asn Asn

130	135	140
Ile Tyr Ile Ser Asp Thr Ser Leu Gln Ser Val Asp Gly Phe Ser Ala		
145	150	155 160
Leu Lys Lys Val Asn Val Phe Asn Val Asn Asn Asn Lys Lys Leu Thr		
	165	170 175
Ser Ile Lys Ser Pro Val Glu Thr Val Ser Asp Ser Leu Gln Phe Ser		
	180	185 190
Phe Asn Gly Asn Gln Thr Lys Ile Thr Phe Asp Asp Leu Val Trp Ala		
	195	200 205
Asn Asn Ile Ser Leu Thr Asp Val His Ser Val Ser Phe Ala Asn Leu		
	210	215 220
Gln Lys Ile Asn Ser Ser Leu Gly Phe Ile Asn Asn Ser Ile Ser Ser		
225	230	235 240
Leu Asn Phe Thr Lys Leu Asn Thr Ile Gly Gln Thr Phe Ser Ile Val		
	245	250 255
Ser Asn Asp Tyr Leu Lys Asn Leu Ser Phe Ser Asn Leu Ser Thr Ile		
	260	265 270
Gly Gly Ala Leu Val Val Ala Asn Asn Thr Gly Leu Gln Lys Ile Gly		
	275	280 285
Gly Leu Asp Asn Leu Thr Thr Ile Gly Gly Thr Leu Glu Val Val Gly		
	290	295 300
Asn Phe Thr Ser Leu Asn Leu Asp Ser Leu Lys Ser Val Lys Gly Gly		
305	310	315 320
Ala Asp Val Glu Ser Lys Ser Ser Asn Phe Ser Cys Asn Ala Leu Lys		
	325	330 335
Ala Leu Gln Lys Lys Gly Gly Ile Lys Gly Glu Ser Phe Val Cys Lys		
	340	345 350
Asn Gly Ala Ser Ser Thr Ser Val Lys Leu Ser Ser Thr Ser Lys Ser		
	355	360 365
Gln Ser Ser Gln Thr Thr Ala Lys Val Ser Lys Ser Ser Ser Lys Ala		
	370	375 380
Glu Glu Lys Lys Phe Thr Ser Gly Asp Ile Lys Ala Ala Ala Ser Ala		

385		390		395		400
Ser Ser Val Ser Ser Ser Gly Ala Ser Ser Ser Ser Ser Lys Ser Ser						
	405		410		415	
Lys Gly Asn Ala Ala Ile Met Ala Pro Ile Gly Gln Thr Thr Pro Leu						
	420		425		430	
Val Gly Leu Leu Thr Ala Ile Ile Met Ser Ile Met						
	435		440			

<210> 23

<211> 3107

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1001)..(2104)

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 attatcatca ttttatatgt taatattcat tgatcctatt acattatcaa tccttgcggt 180
 tcagcttcca ctaatttaga tgactatttt tcatcatttg cgatcatctc taacaccgta 240
 tatgataata tactagtaac gtaaatacta gttagtagat gatagttgat ttttattcca 300
 acagtattta tgttttgtca ttcttttcta cataatcttg aaactaggta gatctacaat 360
 tgaaaagtaa atactaacat tatttactaa atttaagtta gaaatcggca cgaaaaaaat 420
 ttgacagatt acgagagtcc agccaaaata tgagtatatt actatttccc cttggtgaaa 480
 gaaatgaaag atgttatttt ttaccggctt agtaatactg agctacttac ttgggggaaa 540
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 gagcagtatg ctcttcaa at tcgaactttt tgaacatctt tctccacat tcttgatttt 660
 ttcacattca aaacgcgctg tgaagctggt agaaatttac agatcgaggc atatttctat 720
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tctgaccaga agccagactt gaacagttac atattgtgct ttgcagtcgt taaatttccc 840

gaactgtttt cgtatttttt tttcttttcc tcttttccac tggatcagat caaaagccga 900

ctaaaaattt ggcaatttaa agaaagcatc ttttaaagat agaaaagggt atttcaacaa 960

aaaagtatct tttcttcaact tttcttttcaa caattcaaag atg gct aga acc ata 1015
Met Ala Arg Thr Ile
1 5

act ttt gat atc cct tcc caa tat aaa ctc gta gat tta ata ggt gag 1063
Thr Phe Asp Ile Pro Ser Gln Tyr Lys Leu Val Asp Leu Ile Gly Glu
10 15 20

gga gcg tac gga aca gta tgt tca gca att cat aag cct tcc ggc ata 1111
Gly Ala Tyr Gly Thr Val Cys Ser Ala Ile His Lys Pro Ser Gly Ile
25 30 35

aag gta gct atc aag aaa ata caa ccg ttt agc aaa aaa ttg ttt gtt 1159
Lys Val Ala Ile Lys Lys Ile Gln Pro Phe Ser Lys Lys Leu Phe Val
40 45 50

aca aga act ata cgt gag atc aag ctt tta cgg tat ttc cat gaa cac 1207
Thr Arg Thr Ile Arg Glu Ile Lys Leu Leu Arg Tyr Phe His Glu His
55 60 65

gaa aac ata ata agt ata ttg gat aaa gta agg cca gta tcc ata gac 1255
Glu Asn Ile Ile Ser Ile Leu Asp Lys Val Arg Pro Val Ser Ile Asp
70 75 80 85

aaa cta aac gct gtt tat tta gtc gaa gag ttg atg gaa acc gat tta 1303
Lys Leu Asn Ala Val Tyr Leu Val Glu Glu Leu Met Glu Thr Asp Leu
90 95 100

caa aaa gta att aat aat cag aat agc ggg ttt tcc act tta agt gat 1351
Gln Lys Val Ile Asn Asn Gln Asn Ser Gly Phe Ser Thr Leu Ser Asp
105 110 115

gac cat gtt caa tac ttt aca tac caa atc ctc aga gcc tta aag tct 1399
Asp His Val Gln Tyr Phe Thr Tyr Gln Ile Leu Arg Ala Leu Lys Ser
120 125 130

att cac agt gca caa gtt atc cat aga gac ata aag cca tca aac ctg 1447
Ile His Ser Ala Gln Val Ile His Arg Asp Ile Lys Pro Ser Asn Leu
135 140 145

tta cta aat tcc aat tgt gat ctc aaa gtc tgc gat ttt gga cta gcg 1495
Leu Leu Asn Ser Asn Cys Asp Leu Lys Val Cys Asp Phe Gly Leu Ala

150	155	160	165	
agg tgt tta gct agc agt agc gat tca aga gaa aca ttg gta gga ttc				1543
Arg Cys Leu Ala Ser Ser Ser Asp Ser Arg Glu Thr Leu Val Gly Phe				
	170	175	180	
atg acg gag tac gtc gca acg cga tgg tac agg gca ccc gag ata atg				1591
Met Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met				
	185	190	195	
cta act ttt caa gag tac aca act gcg atg gat ata tgg tca tgc gga				1639
Leu Thr Phe Gln Glu Tyr Thr Thr Ala Met Asp Ile Trp Ser Cys Gly				
	200	205	210	
tgc att ttg gct gaa atg gtc tcc ggg aag cct ttg ttc cca ggc aga				1687
Cys Ile Leu Ala Glu Met Val Ser Gly Lys Pro Leu Phe Pro Gly Arg				
	215	220	225	
gac tat cat cat caa tta tgg cta att cta gaa gtc ttg gga act cca				1735
Asp Tyr His His Gln Leu Trp Leu Ile Leu Glu Val Leu Gly Thr Pro				
	230	235	240	245
tct ttc gaa gac ttt aat cag atc aaa tcc aag agg gct aaa gag tat				1783
Ser Phe Glu Asp Phe Asn Gln Ile Lys Ser Lys Arg Ala Lys Glu Tyr				
	250	255	260	
ata gca aac tta cct atg agg cca ccc ttg cca tgg gag acc gtc tgg				1831
Ile Ala Asn Leu Pro Met Arg Pro Pro Leu Pro Trp Glu Thr Val Trp				
	265	270	275	
tca aag acc gat ctg aat cca gat atg ata gat tta cta gac aaa atg				1879
Ser Lys Thr Asp Leu Asn Pro Asp Met Ile Asp Leu Leu Asp Lys Met				
	280	285	290	
ctt caa ttc aat cct gac aaa aga ata agc gca gca gaa gct tta aga				1927
Leu Gln Phe Asn Pro Asp Lys Arg Ile Ser Ala Ala Glu Ala Leu Arg				
	295	300	305	
cac cct tac ctg gca atg tac cat gac cca agt gat gag ccg gaa tat				1975
His Pro Tyr Leu Ala Met Tyr His Asp Pro Ser Asp Glu Pro Glu Tyr				
	310	315	320	325
cct cca ctt aat ttg gat gat gaa ttt tgg aaa ctg gat aac aag ata				2023
Pro Pro Leu Asn Leu Asp Asp Glu Phe Trp Lys Leu Asp Asn Lys Ile				
	330	335	340	
atg cgt ccg gaa gag gag gaa gaa gtg ccc ata gaa atg ctc aaa gac				2071
Met Arg Pro Glu Glu Glu Glu Glu Val Pro Ile Glu Met Leu Lys Asp				

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          345          350          355
atg ctt tac gat gaa cta atg aag acc atg gaa tagtattcac aagaacattt 2124
Met Leu Tyr Asp Glu Leu Met Lys Thr Met Glu
          360          365

ctgccatact tctaaaattt ccctatattc agcttagcag tgacacggtg tggctctgtag 2184
gtcaatatgt aagtaagaaa cttcaactca catatgcacg atgcatgcca atggaaaaat 2244
gcaaggaacg aaatggcgcc acggcaacaa gttttttttt ttcgccagca gaagtacacg 2304
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<210> 24

<211> 368

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

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 20 25 30
 Lys Pro Ser Gly Ile Lys Val Ala Ile Lys Lys Ile Gln Pro Phe Ser
 35 40 45
 Lys Lys Leu Phe Val Thr Arg Thr Ile Arg Glu Ile Lys Leu Leu Arg
 50 55 60
 Tyr Phe His Glu His Glu Asn Ile Ile Ser Ile Leu Asp Lys Val Arg
 65 70 75 80
 Pro Val Ser Ile Asp Lys Leu Asn Ala Val Tyr Leu Val Glu Glu Leu
 85 90 95
 Met Glu Thr Asp Leu Gln Lys Val Ile Asn Asn Gln Asn Ser Gly Phe
 100 105 110
 Ser Thr Leu Ser Asp Asp His Val Gln Tyr Phe Thr Tyr Gln Ile Leu
 115 120 125
 Arg Ala Leu Lys Ser Ile His Ser Ala Gln Val Ile His Arg Asp Ile
 130 135 140
 Lys Pro Ser Asn Leu Leu Leu Asn Ser Asn Cys Asp Leu Lys Val Cys
 145 150 155 160
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 Ile Trp Ser Cys Gly Cys Ile Leu Ala Glu Met Val Ser Gly Lys Pro
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Ser Ser Gly Thr Thr Val Thr Phe Glu Gly Thr Thr Thr Phe Gln Tyr
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Val Val Gly Ala Ser Gly His Thr Ile Asp Gly Gln Gly Ala Lys Trp
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Trp Asp Gly Leu Gly Asp Ser Gly Lys Val Lys Pro Lys Phe Val Lys
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Leu Ala Leu Thr Gly Thr Ser Lys Val Thr Gly Leu Asn Ile Lys Asn
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Ala Pro His Gln Val Phe Ser Ile Asn Lys Cys Ser Asp Leu Thr Ile
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Ser Asp Ile Thr Ile Asp Ile Arg Asp Gly Asp Ser Ala Gly Gly His
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Asn Thr Asp Gly Phe Asp Val Gly Ser Ser Ser Asn Val Leu Ile Gln
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Lys Thr Val Glu Gly Ala Thr Gly Thr Val Thr Asn Val Asn Phe Ile		
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Asp Tyr Leu Asn Ser Lys Thr Thr Gly Thr Ala Thr Gly Gly Val Pro		
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Gln Asp Leu Asn Thr Ala Leu Gly Gln Lys Val Gln Tyr Thr Phe Leu
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Asp Thr Gly Asn Ser Asn Asp Gln Leu Leu His Leu Pro Ser Thr Thr
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Ser Ser Ser Ile Ile Thr Gly Ser Leu Ala Ala Ala Asn Phe Thr Gly
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Ser Ser Ser Ser Ser Ser Ile Pro Lys Val Thr Ser Ser Val Ile Thr
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Ser Ile Asn Tyr Gln Ser Ser Asn Ser Thr Val Val Thr Gln Phe Thr
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Pro Leu Pro Ser Ser Ser Arg Asn Glu Thr Lys Ser Ser Gln Thr Thr
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260

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/08555

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68

US CL : 435/6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1, 91,2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WEST, STN FILES MEDLINE, BIOSIS, CAPLUS, LIFESCI, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----P Y ---- A	US 5,981,207 A (BURBAUM et al.) 09 November 1999, col. 1-2, lines 51-7.	33-35 ---- 1-5, 14, 18, 20-32, 44, 47, 52, 63, 74 ---- 6-13, 15-17, 19, 36-43, 45, 46, 48-51, 53-62, 64-73, 75-83

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

12 JUNE 2000

Date of mailing of the international search report

05 JUL 2000

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet) (July 1998)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/08555

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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A	JOHNSTON, M. et al. Complete Nucleotide Sequence of <i>Saccharomyces cerevisiae</i> Chromosome VIII. <i>Science</i> . 30 September 1994 Vol. 265. Pages 2077-2082.	45, 46, 48, 49-51, 53-62, 64-73, 75-83
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